

EPPER526106 Page 1  
Seq. ID 2 (Claro 63)

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OM protein - protein search, using sw model  
Run on: June 18, 2004, 19:08:03 ; Search time 184 Seconds  
(without alignments)

1395.120 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345  
Sequence: hptelvkvkdaedqlgarvg.....tmdernqiaeigaslikhw 263

Scoring table: BIOSW62  
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976033577 residues

Total number of hits satisfying chosen parameters: 6019581  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:  
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2: /cgn2\_6/ptodata/2/paa/US05\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep:\*

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21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep:\*

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23: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*

24: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep:\*

RESULT 1  
US-09-526-106-2  
; Sequence 2, Application US/09526106  
; GENERAL INFORMATION:  
; APPLICANT: Baint, Robert F.  
; APPLICANT: Baint, Robert F.  
; APPLICANT: Her, Jeng Horng  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Interaction-Activated Proteins  
; FILE REFERENCE: 031167-000700US  
; CURRENT APPLICATION NUMBER: US/09/526,106  
; CURRENT FILING DATE: 2000-03-15  
; PRIORITY APPLICATION NUMBER: US 60/175,968  
; PRIORITY FILING DATE: 1999-03-15  
; PRIORITY APPLICATION NUMBER: US 60/135,926  
; PRIORITY FILING DATE: 1999-05-25  
; PRIORITY APPLICATION NUMBER: US 60/175,968  
; PRIORITY FILING DATE: 2000-01-13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Escherichia coli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
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FEATURE: OTHER INFORMATION: TEM-1 beta-lactamase

US-09-526-106-2

Query Match 98.9%; Score 1330; DB 19; Length 263; Best Local Similarity 98.9%; Pred. No. 5.2e-132; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEIIVKVKAEDQIGARYVYIELDINSCEILESFRSEERFPMMSTFKVLLCGAVLRSID 60  
1 HPEIIVKVKAEDQIGARYVYIELDINSCEILESFRSEERFPMMSTFKVLLCGAVLRSID 60

QY 61 AGOQOLGRIRHYSONDLYVSYPEVKHLDGTMVTRELCSAATMSDNTANLLITIGP 120  
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QY 121 KELTAFLHMGDHTRLDRWEPELNEAIPNDEDTTPAMATRKLTGELTLASRQ 180  
121 KELTAFLHMGDHTRLDRWEPELNEAIPNDEDTTPAMATRKLTGELTLASRQ 180

QY 181 QLIDWMEADKVAGPLRSALPAGFIAMKSGAGERGSRGIIAALGPDKPSRIVVIYTG 240  
181 QLIDWMEADKVAGPLRSALPAGFIAMKSGAGERGSRGIIAALGPDKPSRIVVIYTG 240

QY 241 SQATMDERNRQIAIGASLIKHW 263  
241 SQATMDERNRQIAIGASLIKHW 263

Db 241 SQATMDERNRQIAIGASLIKHW 263

RESULT 2  
US-09-764-163A-2

; Sequence 2, Application US/09764163A  
; GENERAL INFORMATION:  
; APPLICANT: Ballint, Robert F.  
; APPLICANT: Her, Jeng-Horng  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Circularly Permutated, Interaction-Activated Proteins  
; FILE REFERENCE: 021167-00071038  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/175, 968  
; PRIOR APPLICATION NUMBER: US 09/526, 106  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: pdb 1BTL  
; OTHER INFORMATION: Escherichia coli  
; OTHER INFORMATION: TEM-1 beta-lactamase

US-09-764-163A-2

Query Match 98.9%; Score 1330; DB 22; Length 263; Best Local Similarity 98.9%; Pred. No. 5.2e-132; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEIIVKVKAEDQIGARYVYIELDINSCEILESFRSEERFPMMSTFKVLLCGAVLRSID 60  
1 HPEIIVKVKAEDQIGARYVYIELDINSCEILESFRSEERFPMMSTFKVLLCGAVLRSID 60

QY 61 AGOQOLGRIRHYSONDLYVSYPEVKHLDGTMVTRELCSAATMSDNTANLLITIGP 120  
61 AGOQOLGRIRHYSONDLYVSYPEVKHLDGTMVTRELCSAATMSDNTANLLITIGP 120

QY 121 KELTAFLHMGDHTRLDRWEPELNEAIPNDEDTTPAMATRKLTGELTLASRQ 180  
121 KELTAFLHMGDHTRLDRWEPELNEAIPNDEDTTPAMATRKLTGELTLASRQ 180

QY 181 QLIDWMEADKVAGPLRSALPAGFIAMKSGAGERGSRGIIAALGPDKPSRIVVIYTG 240  
181 QLIDWMEADKVAGPLRSALPAGFIAMKSGAGERGSRGIIAALGPDKPSRIVVIYTG 240

QY 241 SQATMDERNRQIAIGASLIKHW 263  
241 SQATMDERNRQIAIGASLIKHW 263

Db 241 SQATMDERNRQIAIGASLIKHW 263

RESULT 3  
US-09-791-537-90233

; Sequence 90233, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791, 537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 90233  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: pdb 1BTL  
; OTHER INFORMATION: US-09-791-537-90233

Query Match 98.9%; Score 1330; DB 22; Length 263; Best Local Similarity 98.9%; Pred. No. 5.2e-132; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEIIVKVKAEDQIGARYVYIELDINSCEILESFRSEERFPMMSTFKVLLCGAVLRSID 60  
1 HPEIIVKVKAEDQIGARYVYIELDINSCEILESFRSEERFPMMSTFKVLLCGAVLRSID 60

QY 61 AGOQOLGRIRHYSONDLYVSYPEVKHLDGTMVTRELCSAATMSDNTANLLITIGP 120  
61 AGOQOLGRIRHYSONDLYVSYPEVKHLDGTMVTRELCSAATMSDNTANLLITIGP 120

QY 121 KELTAFLHMGDHTRLDRWEPELNEAIPNDEDTTPAMATRKLTGELTLASRQ 180  
121 KELTAFLHMGDHTRLDRWEPELNEAIPNDEDTTPAMATRKLTGELTLASRQ 180

QY 181 QLIDWMEADKVAGPLRSALPAGFIAMKSGAGERGSRGIIAALGPDKPSRIVVIYTG 240  
181 QLIDWMEADKVAGPLRSALPAGFIAMKSGAGERGSRGIIAALGPDKPSRIVVIYTG 240

QY 241 SQATMDERNRQIAIGASLIKHW 263  
241 SQATMDERNRQIAIGASLIKHW 263

Db 241 SQATMDERNRQIAIGASLIKHW 263

RESULT 4  
US-10-668-778-2

; Sequence 2, Application US/10668778  
; GENERAL INFORMATION:  
; APPLICANT: Ballint, Robert F.  
; APPLICANT: Her, Jeng-Horng  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Interaction-Activated Proteins  
; FILE REFERENCE: 021167-00070003  
; CURRENT APPLICATION NUMBER: US/10/668, 778  
; CURRENT FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: US/09/526, 106  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: US 60/124, 339  
; PRIOR FILING DATE: 1999-03-15  
; PRIOR APPLICATION NUMBER: US 60/135, 926  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: US 60/175, 968  
; PRIOR FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2

TYPE: PRT  
; ORGANISM: Escherichia coli  
; FEATURE:  
; OTHER INFORMATION: TEM-1 beta-lactamase  
; US-10-668-778-2

Query Match 98.9%; Score 1330; DB 31; Length 263;  
Best Local Similarity 98.9%; Pred. No. 5.2e-132;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 60  
Db 1 HPELVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 60  
QY 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
Db 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
QY 121 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 180  
Db 121 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 180  
QY 181 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 240  
Db 181 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 240  
QY 241 SQATMDERNRQIAEGASLIKHW 263  
Db 241 SQATMDERNRQIAEGASLIKHW 263

RESULT 5  
PCT-US02-12405-523

Sequence 523, Application PC/TUS0212405  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, ROBERT C.  
; APPLICANT: COHEN, EDWARD H.  
; APPLICANT: NASTRI, HORACIO G.  
; APPLICANT: ROOKY, KRISTIN L.  
; APPLICANT: HOET, RENE  
; APPLICANT: HOGGENBOOM, HENDRICUS R. J. M.  
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
; TITLE OF INVENTION: LIBRARIES  
; FILE REFERENCE: DYAX/002 C1P2  
; CURRENT APPLICATION NUMBER: PCT/US02/12405  
; CURRENT FILING DATE: 2002-04-17  
; PRIORITY NUMBER: 05/198, 069  
; PRIORITY FILING DATE: 2000-04-17  
; PRIORITY APPLICATION NUMBER: 09/1837, 306  
; NUMBER OF SEQ ID NOS: 635  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
PCT-US02-12405-523

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 5.2e-132;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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Db 1 HPELVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 60  
QY 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
Db 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
QY 121 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 180  
Db 121 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 180  
QY 181 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 240  
Db 181 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 240  
QY 241 SQATMDERNRQIAEGASLIKHW 263  
Db 241 SQATMDERNRQIAEGASLIKHW 263

RESULT 6  
PCT-US02-17440-7

Sequence 7, Application PC/TUS0217440  
; GENERAL INFORMATION:  
; APPLICANT: Otto, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patrick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-005A  
; CURRENT APPLICATION NUMBER: PCT/US02/17440  
; CURRENT FILING DATE: 1999-08-02  
; CURRENT APPLICATION NUMBER: 09/1129, 611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
PCT-US02-17440-7

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 5.2e-132;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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Db 1 HPELVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 60  
QY 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
Db 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
QY 121 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 180  
Db 121 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 180  
QY 144 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 203  
Db 144 KELTAFLHNGDHVTLDRWEPPELINEATPNDERTTPVAMATTKLTKLGGELTLASRQ 203  
QY 181 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 240  
Db 181 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 240  
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Db 204 QLIDWMEADKVAGPLRSALPAGWFIADKSGAGERSGSGIIAALGPDKPSRIVIYTG 263

RESULT 7  
PCT-US02-12405-523

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Best Local Similarity 98.9%; Pred. No. 6e-132; 2; Indels 0; Gaps 0;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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Db 1 HPELVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 60  
QY 24 HPELVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 83  
Db 24 HPELVVKDAEOLGARGVYIELDINGEELSFRRSERFPMSITFKVILCAVLSRID 83  
QY 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120  
Db 61 AGEBOLGRIRHYSONDLVEYSPTEKHLTDGMTRELCSAITSMSDNTAANLLTIGP 120

CURRENT APPLICATION NUMBER: PCT/US99/17440  
; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; PCT-US99-17440-14

RESULT 9  
US-09-129-611-7  
; Sequence 7, Application US/09129611A  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Batick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/09/129,611A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; US-09-129-611-7

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132; 1; Mismatches 2; Indels 0; Gaps 0;  
Matches 260; Conservative 1; MisMatches 1; Indels 0; Gaps 0;

QY 1 HPETLKVKDAEDQDGLGARVGVYELDINGEILFSRFSRERPPMSTFKVLLCGAVLSRID 60  
QY 24 HPETLKVKDAEDQDGLGARVGVYELDINGEILFSRFSRERPPMSTFKVLLCGAVLSRID 83

Db 61 AGQEQLGRRIHYSQNDLVEYSVTEKHLTDGMTRVLECSAITSMSDNITANLLITIGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSVTEKHLTDGMTRVLECSAITSMSDNITANLLITIGP 143

QY 121 KELTAFLHNMGHVTDRWEPINEALPNDDEDTTVAATTTRKLTGELLTASQ 180  
QY 144 KELTAFLHNMGHVTDRWEPINEALPNDDEDTTVAATTTRKLTGELLTASQ 203

Db 181 QIDWMADKVAGPLRSALPAGFWFLAKSGAERGSRGSGTIAALGPDKPSRIVIYTG 240  
Db 204 QIDWMADKVAGPLRSALPAGFWFLAKSGAERGSRGSGTIAALGPDKPSRIVIYTG 263

RESULT 8  
PCT-US99-17440-21  
; Sequence 21, Application PCT/US99/17440  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Batick, Amy K.  
; APPLICANT: Patrick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: PCT/US99/17440  
; CURRENT FILING DATE: 1999-08-02  
; CURRENT FILING NUMBER: 09/129,611  
; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; PCT-US99-17440-21

Query Match 98.9%; Score 1330; DB 15; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132; 1; Mismatches 2; Indels 0; Gaps 0;  
Matches 260; Conservative 1; MisMatches 1; Indels 0; Gaps 0;

QY 1 HPETLKVKDAEDQDGLGARVGVYELDINGEILFSRFSRERPPMSTFKVLLCGAVLSRID 60  
QY 24 HPETLKVKDAEDQDGLGARVGVYELDINGEILFSRFSRERPPMSTFKVLLCGAVLSRID 83

Db 61 AGQEQLGRRIHYSQNDLVEYSVTEKHLTDGMTRVLECSAITSMSDNITANLLITIGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSVTEKHLTDGMTRVLECSAITSMSDNITANLLITIGP 143

QY 121 KELTAFLHNMGHVTDRWEPINEALPNDDEDTTVAATTTRKLTGELLTASQ 180  
QY 144 KELTAFLHNMGHVTDRWEPINEALPNDDEDTTVAATTTRKLTGELLTASQ 203

Db 181 QIDWMADKVAGPLRSALPAGFWFLAKSGAERGSRGSGTIAALGPDKPSRIVIYTG 240  
Db 204 QIDWMADKVAGPLRSALPAGFWFLAKSGAERGSRGSGTIAALGPDKPSRIVIYTG 263

RESULT 10  
US-09-129-611-14  
; Sequence 14, Application US/09129611A  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Batick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/09/129,611A  
; CURRENT FILING DATE: 1999-08-05  
; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; US-09-129-611-14

Query Match 98.9%; Score 1330; DB 15; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132; 2; Mismatches  
Matches 260; Conservative 1; Indels 0; Gaps 0;

QY 1 HPETLVKVDADOLGARVGYIELDINGSGEILSFRPFRPFMSTKVLGAVSRID 60  
Db 24 HPETLVKVDADOLGARVGYIELDINGSGEILSFRPFRPFMSTKVLGAVSRID 83  
QY 61 AGOBOLGRRIHYSQNDIYEVSPTEKHLTDGMVRELSAITSMSDNIAANLITGGP 120  
Db 84 AGOBOLGRRIHYSQNDIYEVSPTEKHLTDGMVRELSAITSMSDNIAANLITGGP 143  
QY 121 KELTAFLINMGDVTLDRWEPELINEAPNDERDTTPEVAMATTLRKLITGELTASRQ 180  
Db 144 KELTAFLINMGDVTLDRWEPELINEAPNDERDTTPEVAMATTLRKLITGELTASRQ 203  
QY 181 QLIDWMEADKVGAGPLRSALPAGWFLADKSAGERGRSGRGLIAALGPDKPSRIVVYTG 240  
Db 204 QLIDWMEADKVGAGPLRSALPAGWFLADKSAGERGRSGRGLIAALGPDKPSRIVVYTG 263

RESULT 11

US-09-129-611-21

; Sequence 21, Application US/09129611A

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; FILE REFERENCE: 0125-005A

; CURRENT APPLICATION NUMBER: US/09/129,611A

; CURRENT FILING DATE: 1999-08-05

; EARLIER APPLICATION NUMBER: 09/129,611

; EARLIER FILING DATE: 1998-08-05

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 286

; TYPE: PRT  
; ORGANISM: Artificial Sequence

US-09-129-611-21

Query Match 98.9%; Score 1330; DB 15; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132; 2; Mismatches  
Matches 260; Conservative 1; Indels 0; Gaps 0;

QY 1 HPETLVKVDADOLGARVGYIELDINGSGEILSFRPFRPFMSTKVLGAVSRID 60  
Db 24 HPETLVKVDADOLGARVGYIELDINGSGEILSFRPFRPFMSTKVLGAVSRID 83  
QY 61 AGOBOLGRRIHYSQNDIYEVSPTEKHLTDGMVRELSAITSMSDNIAANLITGGP 120  
Db 84 AGOBOLGRRIHYSQNDIYEVSPTEKHLTDGMVRELSAITSMSDNIAANLITGGP 143  
QY 121 KELTAFLINMGDVTLDRWEPELINEAPNDERDTTPEVAMATTLRKLITGELTASRQ 180  
Db 144 KELTAFLINMGDVTLDRWEPELINEAPNDERDTTPEVAMATTLRKLITGELTASRQ 203  
QY 181 QLIDWMEADKVGAGPLRSALPAGWFLADKSAGERGRSGRGLIAALGPDKPSRIVVYTG 240  
Db 204 QLIDWMEADKVGAGPLRSALPAGWFLADKSAGERGRSGRGLIAALGPDKPSRIVVYTG 263

QY 241 SQATMDERNRQIAEIGASLIKW 263  
Db 264 SQATMDERNRQIAEIGASLIKW 286

RESULT 12

US-09-490-070-265

; Sequence 265, Application US/09490070

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Llagger, Vic

; Ge, Laming

; Moroney, Simon

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MAC-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070

; FILING DATE: 24-Jan-2000

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 09/025,769

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9090

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 265:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 265:

; US-09-490-070-265

Query Match 98.9%; Score 1330; DB 18; Length 286;

; Best Local Similarity 98.9%; Pred. No. 6e-132; 2; Mismatches  
Matches 260; Conservative 1; Indels 0; Gaps 0;

QY 1 HPETLVKVDADOLGARVGYIELDINGSGEILSFRPFRPFMSTKVLGAVSRID 60  
Db 24 HPETLVKVDADOLGARVGYIELDINGSGEILSFRPFRPFMSTKVLGAVSRID 83  
QY 61 AGOBOLGRRIHYSQNDIYEVSPTEKHLTDGMVRELSAITSMSDNIAANLITGGP 120  
Db 84 AGOBOLGRRIHYSQNDIYEVSPTEKHLTDGMVRELSAITSMSDNIAANLITGGP 143  
QY 121 KELTAFLINMGDVTLDRWEPELINEAPNDERDTTPEVAMATTLRKLITGELTASRQ 180  
Db 144 KELTAFLINMGDVTLDRWEPELINEAPNDERDTTPEVAMATTLRKLITGELTASRQ 203  
QY 181 QLIDWMEADKVGAGPLRSALPAGWFLADKSAGERGRSGRGLIAALGPDKPSRIVVYTG 240  
Db 204 QLIDWMEADKVGAGPLRSALPAGWFLADKSAGERGRSGRGLIAALGPDKPSRIVVYTG 263

QY 241 SQATMDERNRQIAEIGASLIKW 263

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 13

Sequence 362, Application US/09490070

GENERAL INFORMATION:

APPLICANT: Knapik, Achim  
Pack, Peter  
Tilg, Vic  
Ge, Liming

Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0 (RPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/025,769

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 362:  
US-09-490-070-362

Query Match 98.9%; Score 1330; DB 18; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132; 260; Conservatve 1; Mismatches 2; Indels 0; Gaps 0; Matches 260; Conservatve 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQIGARVGTIELDANSGLIESFRSEERPPMSTPKVILCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQIGARVGTIELDANSGLIESFRSEERPPMSTPKVILCGAVLSRID 60

QY 61 AGQEQIGRGRHYSQNDLVEVSPVTEKHTIDGTMVTRELCSAITSMSINTAANTLLITIGP 120  
Db 84 AGQEQIGRGRHYSQNDLVEVSPVTEKHTIDGTMVTRELCSAITSMSINTAANTLLITIGP 143

Db 121 KELTALPHNMGDHVTLDRMPPELNEAIPNDERDTTPVAMATURKLKGELTLASRQ 180  
Db 144 KELTALPHNMGDHVTLDRMPPELNEAIPNDERDTTPVAMATURKLKGELTLASRQ 203

QY 181 QLIDMEADKAGPLRSALPAGWFADKSAGERSRGITIALGPDKPSRIVIYTG 240  
Db 204 QLIDMEADKAGPLRSALPAGWFADKSAGERSRGITIALGPDKPSRIVIYTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 14

US/09-490-070A-265

Sequence 265, Application US/09490070A

GENERAL INFORMATION:

APPLICANT: Knapik, Achim  
Pack, Peter  
Tilg, Vic  
Ge, Liming

Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandcock, Esq. c/o Heller Rhman  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0 (RPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandcock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-09-490-070A-265

Query Match 98.9%; Score 1330; DB 18; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132; 260; Conservatve 1; Mismatches 2; Indels 0; Gaps 0; Matches 260; Conservatve 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQIGARVGTIELDANSGLIESFRSEERPPMSTPKVILCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQIGARVGTIELDANSGLIESFRSEERPPMSTPKVILCGAVLSRID 60

QY 61 AGQEQIGRGRHYSQNDLVEVSPVTEKHTIDGTMVTRELCSAITSMSINTAANTLLITIGP 120  
Db 84 AGQEQIGRGRHYSQNDLVEVSPVTEKHTIDGTMVTRELCSAITSMSINTAANTLLITIGP 143

QY 121 KELTALPHNMGDHVTLDRMPPELNEAIPNDERDTTPVAMATURKLKGELTLASRQ 180  
Db 144 KELTALPHNMGDHVTLDRMPPELNEAIPNDERDTTPVAMATURKLKGELTLASRQ 203

QY 181 QLIDMEADKAGPLRSALPAGWFADKSAGERSRGITIALGPDKPSRIVIYTG 240  
Db 204 QLIDMEADKAGPLRSALPAGWFADKSAGERSRGITIALGPDKPSRIVIYTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 15  
US-09-490-070A-362  
Sequence 362, Application US/09490070A

GENERAL INFORMATION:  
APPLICANT: Knapik, Achim

Pack, Peter  
Flag, Vic  
Ge, Liming

Moroney, Simon  
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490, 070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-070A-362

Query Match: 98.9%; Score 1330; DB 18; Length 286;

Best Local Similarity 98.9%; Pred. No. 6e-132; Gaps 0;

Matches 260; Conservative 1; Mismatches 2; Indels 0;

Qy 1 RPTETLVKVKDAEDQLGARVGVYIELDINGNSGEILESFSASRERPPMMSTPKVLLGAVNSRID 60

Db 24 RPTETLVKVKDAEDQLGARVGVYIELDINGNSGEILESFSASRERPPMMSTPKVLLGAVNSRID 83

Qy 61 AGQEQQLGRRRHSQNDLVEYSPVTEKELDTGNTVRELSAATMSDNTAANLLTITGGP 120

Db 84 AGQEQQLGRRRHSQNDLVEYSPVTEKELDTGNTVRELSAATMSDNTAANLLTITGGP 143

Qy 121 KELTATLHNMDHVTLDWRPELNEAIPNEDRDTTPVANATURKLTGELLTASQ 180

Db 144 KELTATLHNMDHVTLDWRPELNEAIPNEDRDTTPVANATURKLTGELLTASQ 203

Qy 181 QLIDWMEADKAGPLRSALAGWFLADKSSAGERSRSRGITAALGDGKSSRIVWYTG 240

Db 204 QLIDWMEADKAGPLRSALAGWFLADKSSAGERSRSRGITAALGDGKSSRIVWYTG 263

Qy 241 SQATMDERNRQIAEIGASLIEW 263

Db 264 SQATMDERNRQIAEIGASLIEW 286

Search completed: June 18, 2004, 19:13:52  
Job time : 185 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:30:18 ; Search time 18 Seconds

(without alignments)  
760.803 Million cell updates/sec

Title: EPER526106.PEP

Sequence: 1 hptelvkvdaedqigarvg.....tmderrnqiaeigaslikhw 263

Perfile score: 1345

Scoring table: BiostarM62

Gapop 10.0 , Gapext 0.5

Searched:

141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42;\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID

Query Description

Result No.	Score	Match	Length	DB	ID	Description
1	1325	98.5	286	1	BLAT_ECOLI	BLAT_ECOLI STANDARD; PRT; 286 AA.
2	942	70.0	286	1	BLAT_ECOLI	BLAT_ECOLI P0810 escherichia
3	940	69.9	286	1	BLAT_ECOLI	BLAT_ECOLI P45579 escherichia
4	937	69.7	286	1	BLAT_ECOLI	BLAT_ECOLI Q94244 klebsiella
5	936	69.6	286	1	BLAT_ECOLI	BLAT_ECOLI Q08337 escherichia
6	935	69.5	286	1	BLAT_ECOLI	BLAT_ECOLI P14558 escherichia
7	933	69.4	286	1	BLAT_ECOLI	BLAT_ECOLI Q81656 escherichia
8	932	69.3	286	1	BLAT_ECOLI	BLAT_ECOLI P30896 klebsiella
9	929	69.1	286	1	BLAT_ECOLI	BLAT_ECOLI P37320 klebsiella
10	905	67.3	279	1	BLAT_ECOLI	BLAT_ECOLI P05192 klebsiella
11	879	65.4	260	1	BLAT_ECOLI	BLAT_ECOLI P96348 klebsiella
12	874	65.0	286	1	BLAT_ECOLI	BLAT_ECOLI P18251 enterobacte
13	672	50.0	298	1	BLAT_ECOLI	BLAT_ECOLI P30897 proteus mir
14	573	42.6	304	1	BLAT_ECOLI	BLAT_ECOLI Q44056 aeromonas h
15	539.5	40.1	288	1	BLAT_ECOLI	BLAT_ECOLI P37322 pseudomonas
16	539.5	40.1	288	1	BLAT_ECOLI	BLAT_ECOLI P16897 pseudomonas
17	536.5	39.9	288	1	BLAT_ECOLI	BLAT_ECOLI P81781 vibrio chol
18	535.5	39.8	288	1	BLAT_ECOLI	BLAT_ECOLI P03170 pseudomonas
19	516.5	38.4	290	1	BLAT_ECOLI	BLAT_ECOLI P23954 klebsiella
20	513.5	38.2	291	1	BLAT_ECOLI	BLAT_ECOLI P22391 klebsiella
21	512.5	38.1	293	1	BLAT_ECOLI	BLAT_ECOLI P14171 rhodobacter
22	505.5	37.6	302	1	BLAT_ECOLI	BLAT_ECOLI Q06315 noocardia la
23	498.5	37.1	288	1	BLAT_ECOLI	BLAT_ECOLI Q51355 pseudomas
24	496.5	36.9	294	1	BLAT_ECOLI	BLAT_ECOLI Q01165 yersinia en
25	494.5	36.8	306	1	BLAT_ECOLI	BLAT_ECOLI P35392 streptomyce
26	490	36.4	291	1	BLAT_ECOLI	BLAT_ECOLI Q47066 escherichia
27	489.5	36.4	305	1	BLAT_ECOLI	BLAT_ECOLI P33949 haemophilus
28	487	36.2	291	1	BLAT_ECOLI	BLAT_ECOLI P74841 salmonella
29	486.5	36.2	267	1	BLAT_ECOLI	BLAT_ECOLI P80545 serratio
30	483.5	35.9	306	1	BLAT_ECOLI	BLAT_ECOLI P39824 bacillus su
31	483	35.9	314	1	BLAT_ECOLI	BLAT_ECOLI P14560 streptomyce
32	482.5	35.9	306	1	BLAT_ECOLI	BLAT_ECOLI Q44674 bacillus am
33	477	35.5	291	1	BLAT_ECOLI	BLAT_ECOLI P28585 escherichia

ALIGNMENTS

34	476	35.4	303	1	BLA2_XANMA	P96465 xanthomonas
35	474	35.2	291	1	BLC2_SALTY	Q38070 salmonella
36	471.5	35.1	294	1	BLC2_CITDI	P22390 citrobacter
37	471	35.0	291	1	BLC5_SALTY	Q65975 salmonella
38	467.5	34.8	309	1	BLA7_BACTU	Q45726 bacillus th
39	467	34.7	291	1	BLC6_SALTY	Q65976 salmonella
40	466.5	34.7	311	1	BLA2_STRCI	Q06650 streptomyce
41	462	34.3	325	1	BLA1_STRCI	Q3680 streptomyce
42	459.5	34.2	305	1	BLAC_STRLA	P35393 streptomyce
43	458.5	34.1	294	1	BLAF_MYCF0	Q59517 mycobacteri
44	455	33.9	305	1	BLAC_BACCE	P0809 bacillus ce
45	455.5	33.9	306	1	BLA1_BACME	P28018 bacillus ce





FT	STRAND	113	114	RT	pneumoniae isolates from patients in an intensive care unit in	
FT	HELIX	115	124	RT	Amsterdam.;"	
FT	HELIX	128	137	RL	Antimicrob. Agents Chemother. 44:1081-1084 (2000).	
FT	TURN	138	139	CC	-I- FUNCTION: Broad spectrum beta-lactamase which hydrolyzes	
FT	HELIX	140	150	CC	penicillins, as well as cephalosporins except cephalexin. Also	
FT	TURN	151	152	CC	hydrolyzes aztreonam, but not imipenem. Confers high resistance	
FT	STRAND	157	157	CC	to ceftazidime, cefotaxime, aztreonam and piperacillin.	
FT	TURN	162	163	CC	-I- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-	
FT	HELIX	164	165	CC	amino acid.	
FT	TURN	170	171	CC	-I- ENZYME REGULATION: Inhibited 16-fold better by the beta-lactamase	
FT	TURN	174	175	CC	inhibitor clavulanic acid than by tazobactam.	
FT	STRAND	176	177	CC	-I- SIMILARITY: Belongs to the class-A beta-lactamase family.	
FT	HELIX	179	191	CC	-----	
FT	TURN	193	194	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
FT	HELIX	197	208	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
FT	TURN	209	209	CC	the European Bioinformatics Institute. There are no restrictions on its	
FT	HELIX	214	220	CC	use by non-profit institutions as long as its content is in no way	
FT	TURN	223	224	CC	modified and this statement is not removed. Usage by and for commercial	
FT	STRAND	226	233	CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> )	
FT	TURN	236	237	CC	or send an email to license@isb-sib.ch).	
FT	STRAND	239	246	CC	-----	
FT	TURN	248	249	CC	-----	
FT	STRAND	253	260	CC	-----	
FT	HELIX	266	282	CC	-----	
FT	TURN	283	283	CC	-----	
SEQUENCE	286 AA;	31224 MW;	C78F42667E698B6C CRC64;	DR	HSSP; P14557; ISHW;	
Query	Match	70.0%	Score 942;	DB 1;	InterPro; IPR000811; Beta_lactamase;	
Best	Local Similarity	68.3%	Length 286;	DR	InterPro; IPR00144; beta-lactamase_1.	
Matches	179;	Conservative	Pred. No. 1.5e-67;	DR	PRINTS; PR0018; BLACTAMASE.	
QY	2	PETLVKVKQEDQIGARVGVYIELDINSGTLESRSEERPPMSMSTPKVUICGAVSRIDA	61	DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.	
Db	23	PQPLRQIKULSESQLSGRGVGMIEMLDLASGRITLTANRADERPPMSIPIFKVUICGAVLRVDA	82	DR	HYDROLASE; Antibiotic resistance_Signal; Plasmid.	
QY	62	GQEQLGRHRHYSQNDLIVESPVTKEHLITQDMTIVBLCSAITMSDNTAANLLITIGGPK	121	FT	SIGNAL 1 21 POTENTIAL.	
Db	83	GDEQLERKHYRQDQLDVDPSPVSEKHLADGMTCVGLCAAAITMSDNSAANLLATVGGPA	142	FT	CHAIN 22 286 BETA-LACTAMASE SHV-13.	
QY	122	ELTAAHNMGDHVTRLDWRPNEALPNDERTTPVAMATURKLGELLTASRQ	181	FT	ACT_SITE 66 66 BY SIMILARITY.	
Db	143	GLTAFLRQIGDNVTRLDWRPNEALPNDERTTPVAMATURKLGELLTASRQ	202	FT	DISULFID 73 119 BY SIMILARITY.	
QY	182	LIDWMEADKVAGPLRSALPAGWFTADKSGAGERSRGRTAALGPDGKPSRIVVYTGS	241	FT	BINDING 230 232 SUBSTRATE (BY SIMILARITY).	
Db	203	LIQWMVDDRVAGPLRSVPLAGWFTADKIGAGERGARGIVALLGPNPKAARIWVYLRT	262	SEQUENCE	286 AA;	C78F426DA3FF5502 CRC64;
QY	242	QATMDMRNQTAEGASLIKW	263	Query Match	69.9%; Score 940; DB 1; Length 286;	
Db	263	PASMAERNQQIAGIGALIHW	284	Best	Local Similarity 67.9%; Pred. No. 2.1e-67;	
RESULT 3	BL13_KLEPN	STANDARD;	PRT;	Matches	178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;	
ID	BL13_KLEPN	STANDARD;	PRT;	286 AA.	QY 2 PETLVKVKQEDQIGARVGVYIELDINSGTLESRSEERPPMSMSTPKVUICGAVSRIDA	
AC	Q9S474;				61	
DT	2001 (Rel. 40, Created)				Db 23 PQPLRQIKULSESQLSGRGVGMIEMLDLASGRITLTANRADERPPMSIPIFKVUICGAVLRVDA	
DT	16-OCT-2001 (Rel. 40, Last sequence update)				82	
DT	2003 (Rel. 41, Last annotation update)				QY 62 GQEQLGRHRHYSQNDLIVESPVTKEHLITQDMTIVBLCSAITMSDNTAANLLITIGGPK	
DE	Beta-lactamase SHV-13 precursor (EC 3.5.2.6).				121	
GN	BLA OR SHV13.				Db 83 GDEQLERKHYRQDQLDVDPSPVSEKHLADGMTCVGLCAAAITMSDNSAANLLATVGGPA	
OS	Klebsiella pneumoniae.				142	
OG	Plasmid.				QY 122 ELTAAHNMGDHVTRLDWRPNEALPNDERTTPVAMATURKLGELLTASRQ	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				181	
OC	Enterobacteriaceae; Klebsiella.				Db 143 GLTAFLRQIGDNVTRLDWRPNEALPNDERTTPVAMATURKLGELLTASRQ	
OX	NCBI_TAXID:37;				202	
RN	[1]				QY 182 LIDWMEADKVAGPLRSALPAGWFTADKSGAGERSRGRTAALGPDGKPSRIVVYTGS	
RP	SEQUENCE FROM N.A.				241	
RC	STRAIN=803;				Db 203 LIQWMVDDRVAGPLRSVPLAGWFTADKIGAGERGARGIVALLGPNPKAARIWVYLRT	
RX	MEDLINE=20187177; PubMed=10722518;				262	
RA	Vuan M., Hall L.M.C., Savelkoul P.H.M., Vandebroucke-Grauls C.M.J.E., Livermore D.M.;				QY 242 QATMDMRNQTAEGASLIKW	
RA	DLivermore D.M., a novel extended-spectrum beta-lactamase, in Klebsiella				263 PASMAERNQQIAGIGALIHW	
RT	"SHV-13, a novel extended-spectrum beta-lactamase, in Klebsiella				284	

OX NCBI\_TAXID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9720966; PubMed=9056008;  
 RA Rasheed J.K., Jay C., Metchock B., Berkowitz F., Weigel L.,  
 RA Crellin J., Stewart C., Hill B., Medeiros A.A., Tenoer F.C.;  
 RT "Evaluation of extended-spectrum beta-lactam resistance (SHV-8) in a  
 strain of *Escherichia coli* during multiple episodes of bacteremia.;"  
 RT Antimicrob. Agents Chemother. 41:647-653(1997).  
 RL CC -!- FUNCTION: SHV ENZIMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS  
 CC NOTABLY CEFOTAXIME AND CEPHALIDIME.  
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid.  
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; U92041; AA051384.1; -  
 DR DR Interpro; P14557; ISM;  
 DR Interpro; IPR000871; Beta\_lactamase\_A.  
 DR DR PRINTS; P00144; beta-lactamase; 1.  
 DR DR PRINTS; P00118; BLACTAMASE.  
 DR DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
 KW Hydrolase; Antibiotic\_Resistance\_Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 286 BETA-LACTAMASE SHV-8.  
 FT ACT\_SITE 66 66 BY SIMILARITY.  
 FT DISULFID 73 119 BY SIMILARITY.  
 FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).  
 SQ SEQUENCE 286 AA; 31223 MW; F15990BCBFF5504 CRC64;  
 Query Match 69.7%; Score 937; DB 1; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 3.7e-67;  
 Matches 178; Conservative 39; Mismatches 0; Gaps 0;  
 QY 2 PETLVKVKDAEDOLGARVYIELDINSELISFRSERPMSKFLKLGAVLSRIDA 61  
 23 PPOLEQKLESQESLGSRVGMIEMLDASGRTLTAWRDERPFRPMSTKQVLLCQAVLRAVDA 82  
 QY 62 GQQLGRRIHYSNDLYEVSPTVKEHTDGMTWRELCSAATMSDNPAANLUTTGGPK 121  
 Db 83 GQBLERKHKHQDQDLYDPSKEXKHADGTVGELCAAMTSNSAANLUTVQGP 142  
 QY 122 EELAFLHNGDVTLDPRWEPELNEAIPNDEDTTPTVAMATTLRKLTGELITLASRQ 181  
 143 GLTAFLRQIQLGDVNTRLDWETELNEALPGDARNTTTASMAATRKLTQSLRSQRQ 202  
 QY 182 LIDWMRAKQVAPLRSALPAGFLAKSGAERGSGIQLALGPDKPSRQWVITGS 241  
 Db 203 LQOMWVDRVAGPLRSLVTPAGMFIAKDTGAGERGARGIVALLGPNNKAERIVWYLDT 262  
 QY 242 QATMDERNRQIAIGASLIKHW 263  
 Db 263 PASMARNQQLAGIGAALJEW 284  
 RESULT 5  
 BLA2\_ECOLI STANDARD; PRT; 286 AA.  
 ID BLA2\_ECOLI STANDARD; PRT; 286 AA.  
 AC P14558;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Beta-lactamase SHV-2 precursor (EC 3.5.2.6) (SHV-2A).  
 OS *Escherichia coli*.

OS Klebsiella pneumoniae, (subsp. ozaenae), and  
 OS *Klebsiella pneumoniae* (subsp. ozaenae), and  
 OS *Salmonella typhimurium*.  
 OG Plasmid PBWH77, Plasmid pZM1, Plasmid pB60-1, and Plasmid pM1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Escherichia*.  
 OX NCBI\_TAXID=562, 573, 574, 602;  
 RN [1]  
 RP SEQUENCE OF 22-286.  
 RC SPECIES=S.coli; STRAIN=A2302; PLASMID=PBWH77;  
 RX MEDLINE=9819538; PubMed=3129309;  
 RA Bartelheimer M., Peduzzi J., Yaghane H.B., Labia R.;  
 RT "Single amino acid substitution between SHV-1 beta-lactamase and  
 RT cefotaxime-hydrolyzing SHV-2 enzyme.;"  
 RL FEBS Lett. 231:217-220(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.pneumoniae;  
 RX MEDLINE=90264317; PubMed=2160941;  
 RA Lee K.Y., Hopkins J.D., Syrjanen M.;  
 RT "Direct involvement of IS26 in an antibiotic resistance operon.;"  
 RL J. Bacteriol. 172:3229-3236(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.pneumoniae; STRAIN=KPR 14; PLASMID=pZM1;  
 RX MEDLINE=91237319; PubMed=303379;  
 RA Podbielski A., Schoenling J., Melzer B., Warnatz K., Leusch H.G.;  
 RT "Molecular characterization of a new plasmid-encoded SHV-type beta-  
 RT lactamase (SHV-2 variant) conferring high-level cefotaxime resistance  
 RT upon *Klebsiella pneumoniae*."  
 RL J. Gen. Microbiol. 137:569-578(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.pneumoniae; STRAIN=KPPU-3;  
 RX MEDLINE=96100740; PubMed=486999;  
 RA Nuesch-Abdalla M., Hachler H., Kyser F.H.;  
 RT "New system based on site-directed mutagenesis for highly accurate<sup>2</sup>  
 RT comparison of resistance levels conferred by SHV beta-lactamases.;"  
 RL Antimicrob. Agents Chemother. 39:1726-1730(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.pneumoniae; STRAIN=KPLA-10;  
 RX MEDLINE=97791235; PubMed=145849;  
 RA Nuesch-Abdalla M., Kyser F.H., Hachler H.;  
 RT "Survey and molecular genetics of SHV beta-lactamases in  
 RT Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and  
 RT SHV-12.;"  
 RL Antimicrob. Agents Chemother. 41:943-949(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.ozaenae; STRAIN=2180;  
 RX MEDLINE=90370479; PubMed=3395654;  
 RA Podbielski A., Melzer B.;  
 RT "Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase  
 RT (bla<sub>SHV-2</sub>) of *Klebsiella ozaenae*.;"  
 Nucleic Acids Res. 18:4916-4916(1990).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC PLASMID=PBP60-1;  
 RX MEDLINE=91136192; PubMed=2285285;  
 RA Huletcky A., Culture F., Devesque R.C.;  
 RT "Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.;"  
 RL Antimicrob. Agents Chemother. 34:1725-1732(1990).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium; PLASMID=pHT1;  
 RX MEDLINE=9035111; PubMed=9201259;  
 RA Garbarg-Chenon A., Godard V., Labia R., Nicolas J.C.;  
 RT "Nucleotide sequence of SHV-2 beta-lactamase gene.;"  
 RL Antimicrob. Agents Chemother. 34:1444-1446(1990).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.coli; STRAIN=JC2296;

RA Bradford P.A.;  
 RT "automated thermal cycling is superior to traditional methods for  
 RT nucleotide sequencing of *blshv* genes.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: This enzyme hydrolyzes cefotaxime, cefazidime and other  
 CC broad spectrum cephalosporins.  
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid.  
 CC -!- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. DIFFERS  
 CC IN ONLY ONE POSITION FROM SHV-1.  
 CC  
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 CC  
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
 CC  
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 CC  
 DR EMBL; X62115; CAA44025.1; -.  
 DR EMBL; X53433; CAA37524.1; -.  
 DR EMBL; X53817; CAA37813.1; -.  
 DR EMBL; X54314; CAA39058.1; -.  
 DR EMBL; J47119; AAT5015.1; -.  
 DR EMBL; X58102; CAA66730.1; -.  
 DR EMBL; AFT48851; AAD37413.1; -.  
 DR PIR; A44998; A44998.  
 DR HSSE; P44557; ISHV.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR PF001144; beta-lactamase; 1.  
 DR PRINTS; PR00118; BLaCTAMASE.  
 DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
 KW Hydrolase; Antibiotic\_resistance; Plasmid; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 286 BETA-LACTAMASE SHV-2.  
 FT ACT\_SITE 66 66 BY SIMILARITY.  
 FT DISUFD 73 119 BY SIMILARITY.  
 FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).  
 FT VARIANT 31 31 L->Q (IN SHV-2A).  
 SQ SEQUENCE 286 AA; 3116 MW; 584990BC80BAFF CRC64;  
 Query Match 69.6%; Score 936; DB 1; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 4.4e-67;  
 Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;  
 QY 2 PFTLVKVKDAEDQLGARVGVYIELDINGEELIESFSEBSERPPMSTFKVLLGAVLSRIDA 61  
 Db 23 PQQPEQIKLSEQLSLSGRGVIMEMDLASGRITAWRADERPPMSTFKVLLGAVLARVIDA 82  
 QY 62 GQEOGLRRHYSQNDLVEYSVTPEKLTGDMVRELSAATMSONTAANLLTIGGPK 121  
 Db 83 GDEQLERKIHHRQDQDVYDPEVSEKELADGTVGELCAATMSDANSANILLATVGGA 142  
 QY 122 ELTAFLAHNMGDHVTDRWEPENEALPNDERTTPVAMATRKLTGELTLASRQQ 181  
 Db 143 GLTAFLRQIGDNVTRDRWETEINALPQGDARDTTPASMAITRKLTQSLRSRQ 202  
 QY 182 LIDWMEADKVAGPLSLASALPGWFLADKSGAGERSRGIGIAALGPGKPSRIVVYTGS 241  
 Db 203 LIQWQWVDRVAGPLRSVLPAGWFLADKTAGTGAERGARGIVALLGPNNKAERIVVYLRT 262  
 QY 242 QATMDERNRQTAEGASLIKW 263  
 Db 263 PASMARNQTAGIGAHLIEW 284  
 Query Match 69.5%; Score 935; DB 1; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 5.3e-67;  
 Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;  
 QY 2 PETLVKVKDAEDQLGARVGVYIELDINGEELIESFSEBSERPPMSTFKVLLGAVLSRIDA 61  
 Db 23 PQQPEQIKLSEQLSLSGRGVIMEMDLASGRITAWRADERPPMSTFKVLLGAVLARVIDA 82  
 QY 62 GQEOGLRRHYSQNDLVEYSVTPEKLTGDMVRELSAATMSONTAANLLTIGGPK 121  
 Db 83 GDEQLERKIHHRQDQDVYDPEVSEKELADGTVGELCAATMSDANSANILLATVGGA 142  
 QY 122 ELTAFLAHNMGDHVTDRWEPENEALPNDERTTPVAMATRKLTGELTLASRQQ 181  
 Db 143 GLTAFLRQIGDNVTRDRWETEINALPQGDARDTTPASMAITRKLTQSLRSRQ 202  
 QY 182 LIDWMEADKVAGPLSLASALPGWFLADKSGAGERSRGIGIAALGPGKPSRIVVYTGS 241  
 Db 203 LIQWQWVDRVAGPLRSVLPAGWFLADKTAGTGAERGARGIVALLGPNNKAERIVVYLRT 262  
 QY 242 QATMDERNRQTAEGASLIKW 263  
 Db 263 PASMARNQTAGIGAHLIEW 284  
 RESULT 6  
 B124\_ECOLI STANDARD; PRT; 286 AA.  
 ID B124\_ECOLI  
 AC Q9SI62;  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Beta-lactamase SHV-24 precursor (EC 3.5.2.6).  
 GN BLA OR SHV24.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 NCBI\_TAXID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HK1741;  
 RA Kurokawa H., Yagi T., Shibata N., Araikawa Y.;  
 RT "New SHV-derived extended-spectrum beta-lactamase gene.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: SHV ENZYMES HYDROLIZE BROAD SPECTRUM CEPHALOSPORINS  
 CC NOTABLY CEPOTAXIME AND CEFTAZIDIME.  
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid.  
 CC  
 DR EMBL; X62115; CAA44025.1; -.  
 DR EMBL; X53433; CAA37524.1; -.  
 DR EMBL; X53817; CAA37813.1; -.  
 DR EMBL; X54314; CAA39058.1; -.  
 DR EMBL; J47119; AAT5015.1; -.  
 DR EMBL; X58102; CAA66730.1; -.  
 DR EMBL; AFT48851; AAD37413.1; -.  
 DR PIR; A44998; A44998.  
 DR HSSE; P44557; ISHV.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR InterPro; IPR000871; Beta\_lactamase\_A.  
 DR PF001144; beta-lactamase; 1.  
 DR PRINTS; PR00118; BLaCTAMASE.  
 DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
 KW Hydrolase; Antibiotic\_resistance; Plasmid; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 286 BETA-LACTAMASE SHV-2.  
 FT ACT\_SITE 66 66 BY SIMILARITY.  
 FT DISUFD 73 119 BY SIMILARITY.  
 FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).  
 FT VARIANT 31 31 L->Q (IN SHV-2A).  
 SQ SEQUENCE 286 AA; 3116 MW; 584990BC80BAFF CRC64;  
 Query Match 69.5%; Score 935; DB 1; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 5.3e-67;  
 Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;  
 QY 2 PETLVKVKDAEDQLGARVGVYIELDINGEELIESFSEBSERPPMSTFKVLLGAVLSRIDA 61  
 Db 23 PQQPEQIKLSEQLSLSGRGVIMEMDLASGRITAWRADERPPMSTFKVLLGAVLARVIDA 82  
 QY 62 GQEOGLRRHYSQNDLVEYSVTPEKLTGDMVRELSAATMSONTAANLLTIGGPK 121  
 Db 83 GDEQLERKIHHRQDQDVYDPEVSEKELADGTVGELCAATMSDANSANILLATVGGA 142  
 QY 122 ELTAFLAHNMGDHVTDRWEPENEALPNDERTTPVAMATRKLTGELTLASRQQ 181  
 Db 143 GLTAFLRQIGDNVTRDRWETEINALPQGDARDTTPASMAITRKLTQSLRSRQ 202  
 QY 182 LIDWMEADKVAGPLSLASALPGWFLADKSGAGERSRGIGIAALGPGKPSRIVVYTGS 241  
 Db 203 LIQWQWVDRVAGPLRSVLPAGWFLADKTAGTGAERGARGIVALLGPNNKAERIVVYLRT 262  
 QY 242 QATMDERNRQTAEGASLIKW 263  
 Db 263 PASMARNQTAGIGAHLIEW 284  
 RESULT 7  
 BLA3\_KLEPN STANDARD; PRT; 286 AA.  
 ID BLA3\_KLEPN  
 AC P30856;  
 DT 01-JUL-1993 (Rel. 25, Created)

DT 01-JUL-1993 (Rel. 26, last sequence update)  
 DT 10-OCT-2003 (Rel. 42, last annotation update)  
 DE Beta-lactamase SHV-3 precursor (EC 3.5.2.6).  
 GN BLA OR SHV3.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90146253; PubMed=2624951;  
 RA Nicolas M.H., Jarlier V., Honore N., Philippon A., Cole S.T.;  
 RT "Molecular characterization of the gene encoding SHV3 beta-lactamase  
 responsible for transferable cefotaxime resistance in clinical  
 isolates of Klebsiella pneumoniae";  
 RL Antimicrob. Agents Chemother. 33:2096-2100(1989).  
 CC -!- FUNCTION: This enzyme hydrolyzes cefotaxime, ceftazidime and other  
 broad spectrum cephalosporins.  
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid.  
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
 PTR: A37200; A37200.  
 DR HSSP; P14557; ISHV.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR InterPro; IPR000871; Beta\_lactamase\_A.  
 DR Pfam; PF00144; beta-lactamase; 1.  
 DR PRINTS; PRO0118; BLACTAMASE.  
 DR KW Hydrolase; Antibiotic\_resistance; Plasmid; Signal.  
 FT CHAIN 1 21  
 FT ACT\_SITE 66 66  
 FT DISULFID 73 119  
 FT BINDING 230 232  
 SQ 286 AA; 31211 MW; 82715D986508F50D CRC64;  
 Query Match 69.4%; Score 933; DB 1; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 7.7e-67;  
 Matches 178; Conservative 37; Mismatches 47; Indels 0; Gaps 0;  
 QY 2 PETLVKVDADOLGARYGYIEFDLNSGELIESFRSEERPFPMSTFKVLLGAVLRSIDA 61  
 DR 23 POPENQKLSEESQSGRGMIDASRTITWRAERPFAMSTFKVLLGAVLRSIDA 82  
 QY 62 GQEQLGRHRYYSQNDIVEYSVTEKHLTDGMTRVRECSAATMSDNTAANLITTGIGPK 121  
 DR 83 GDEQERKIRHYQODLVDYSPVSEKHLADGMVGLCAAAITMSDNTAANLITVGGPA 142  
 QY 122 EULAFHMGHDYTRLWRPEPEAFLPNEDDTTVAARTLRLKLTGELITASRQ 181  
 DR 143 GITAFLRQIGDNYTRLDRWETELNEALPGDARDTTPSAMAATRKILTSQRLSARSQLO 202  
 QY 182 LIDWMEADKVAGPLLSALPAGMFIADKSGAGRGSRGIGTAAIGPDGKPSRIVVWVIGS 241  
 DR 203 LIQWMDVDRVAPLRLPSVLPAGWEIANKTGASERGARGIVVALGPNNKAERIVWVYRDT 262  
 QY 242 QATMDERNRQQAEGASLKH 263  
 DR 263 PASHAERNQQTAGIGALIHW 284  
 RESULT 8  
 ID BLA5\_KLEPN  
 ID BLA5\_KLEPN STANDARD; PRT; 286 AA.  
 AC P37320;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-lactamase SHV-5 precursor (EC 3.5.2.6).  
 GN BLA OR SHV5.  
 OS Klebsiella pneumoniae, and  
 OS Pseudomonas aeruginosa.  
 OG Plasmid pPAG-KE.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573, 287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91207045; PubMed=2088203;  
 RA Billot-Klein D., Gutmann L., Collatz E.;  
 RT "Nucleotide sequence of the SHV-5 beta-lactamase gene of a Klebsiella  
 pneumoniae plasmid.";  
 RL Antimicrob. Agents Chemother. 34:2439-2441(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES-K\_pneumoniae; STRAIN=KRBG-2, and KPLA-4;  
 MEDLINE-97291235; Published=9145849;  
 RA Nuesch-Emtirbinen M., Kaiser F.H., Hachler H.;  
 RT Survey and molecular genetics of SHV beta-lactamases in  
 Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and  
 SHV-12. ";  
 RL Antimicrob. Agents Chemother. 41:943-949(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES-P\_aeruginosa;  
 RA Scoulia E., Aranbay A., Tselenitis I.;  
 RT "extended spectrum beta-lactamase SHV-5 in Pseudomonas aeruginosa  
 clinical strain.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS  
 CC NOTABLY CEFOTAXIME AND CEFTAZIDIME. SHV-5 CAUSES PARTICULARLY HIGH  
 CC LEVELS OF RESISTANCE TO AZtreonam AND CEFTAZIDIME.  
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid  
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
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 DR EMBL; X55640; CA39164.1; --.  
 DR EMBL; X98103; CA66731.1; --.  
 DR EMBL; X98104; CA66732.1; --.  
 DR EMBL; AF096930; AAC4608.1; --.  
 DR PIR; A60632; A60632.  
 DR HSSP; P14557; ISHV.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR InterPro; IPR000871; Beta\_lactamase\_A.  
 DR Pfam; PF00144; beta-lactamase; 1.  
 DR PRINTS; PRO0118; BLACTAMASE.  
 DR PROSITE; PS0016; BLACTAMASE.  
 DR KW Hydrolase; Antibiotic\_resistance; Plasmid; Signal.  
 FT CHAIN 1 21  
 FT ACT\_SITE 66 66  
 FT DISULFID 73 119  
 FT BINDING 230 232  
 SQ 286 AA; 31253 MW; 7381426CC51F5FBA CRC64;  
 Query Match 69.3%; Score 932; DB 1; Length 286;  
 Best Local Similarity 67.6%; Pred. No. 9.2e-67;  
 Matches 177; Conservative 39; Mismatches 46; Indels 0; Gaps 0;  
 QY 2 PETLVKVDADOLGARYGYIEFDLNSGELIESFRSEERPFPMSTFKVLLGAVLRSIDA 61  
 DR 23 POPENQKLSEESQSGRGMIDASRTITWRAERPFAMSTFKVLLGAVLRSIDA 82  
 QY 62 GQEQLGRHRYYSQNDIVEYSVTEKHLTDGMTRVRECSAATMSDNTAANLITTGIGPK 121  
 DR 83 GDEQERKIRHYQODLVDYSPVSEKHLADGMVGLCAAAITMSDNTAANLITVGGPA 142

QY	122	ELTAFLHNNGDHTVRLDRMEPEANAEIPNDERDTTPVAMATTKLKIJTGELITLARQQ	181	QY	242	QATMDERNQIAEIGASILKHW	263
Db	143	GLTAFLRQIGDNTVRLDRMEPEANAEIPNDERDTTPVAMATTKLKIJTGELITLARQQ	202	Db	242	PASMAERIQAGIGAILEHW	263
QY	182	LIDWMEADKVAGPLRSALPGWFLADKSGAGERSRGIIAALGPGKPSIIVWYTGS	241	QY	242	QATMDERNQIAEIGASILKHW	263
Db	203	LIDQWMDVDRVAGPLRSVLPAGMFLADKIGASKRGARGIVALIGPNNAERIVVYLDT	262	Db	242	PASMAERIQAGIGAILEHW	263
QY	242	QATMDERNQIAEIGASILKHW	263	QY	242	QATMDERNQIAEIGASILKHW	263
Db	263	PASVAERNOQIAGIGAILEHW	284	Db	242	PASMAERIQAGIGAILEHW	263
RESULT	9			RESULT	10		
BLA4_KLEPN		STANDARD;	PRT;	BLA4_KLEPN		STANDARD;	PRT;
ID				ID			
AC				AC			
P37323;				P05152;			
DT				DT			
01-OCT-1994	(Rel. 30, Created)			13-AUG-1987	(Rel. 05, Last annotation update)		
DT				DT			
16-OCT-2001	(Rel. 40, Last annotation update)			01-OCT-1994	(Rel. 30, Last annotation update)		
DE				DE			
DETA-lactamase SHV-4	(EC 3.5.2.6) (Ceftazidimase 5) (CAZ-5).			Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).			
GN				OC			
BLA OR SHV4.				Enterobacteriaceae; Klebsiella.			
OS				NCBI_TaxID=573;			
OG				NCBI_TaxID=573;			
OC				RN	[1]		
OC				RP			
Enterobacteriaceae; Klebsiella.				SEQUENCE FROM N.A.			
OX				RC			
NCBI_TaxID=573;				SEQUENCE FROM N.A.			
RN				STRAIN=LEN-1;			
RP				MEDLINE-B87030906; PubMed=3533626;			
RT				RA			
ceftazidime of plasmid-mediated SHV-type CAZ-5 beta-lactamase."				Arakawa Y., Ohta M., Kido N., Fujii Y., Komatsu T., Kato N.;			
RL				beta-lactamase gene of Klebsiella pneumoniae and the TEM			
Anti-microb. Agents Chemother. 33:2160-2163 (1989).				beta-lactamase gene mediated by R plasmids.;"			
CC				RT			
NOTABLY CEPHALOTAXIME AND CEFTAZIDIME. SHV-4 CAUSES PARTICULARLY HIGH				FEBS Lett. 207:69-74 (1986).			
LEVELS OF RESISTANCE TO AZTREONAM AND CEFTAZIDIME.				-!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-			
CC				amino acid.			
-!- SIMILARITY: Belongs to the class-A beta-lactamase family.				-!- SIMILARITY: Belongs to the class-A beta-lactamase family.			
CC				-----			
CC				CC			
CC				This SWISS-prote entry is copyright. It is produced through a collaboration			
CC				between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC				the European Bioinformatics Institute. There are no restrictions on its			
CC				use by non-profit institutions as long as its content is in no way			
CC				modified and this statement is not removed. Usage by and for commercial			
CC				entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC				or send an email to license@isb-sib.ch).			
CC				-----			
DR				CC			
HSSP; P14557; ISHV.				DR			
DR				InterPro; IPR001466; Beta_lactamase.			
InterPro; IPR001466; Beta_lactamase.				DR			
DR				InterPro; IPR000871; Beta_lactamase_A.			
InterPro; IPR000871; Beta_lactamase_A.				DR			
DR				Pfam; PF00144; beta-lactamase; 1.			
Pfam; PF00144; beta-lactamase; 1.				DR			
DR				PRINTS; PR0018; BBLACTAMASE.			
PRINTS; PR0018; BBLACTAMASE.				DR			
DR				PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
PROSITE; PS00146; BETA_LACTAMASE_A; 1.				DR			
DR				KW			
KW				Hydrolase; Antibiotic resistance; Signal.			
Hydrolase; Antibiotic resistance; Plasmid.				FT			
ACT_SITE	45	45	BY SIMILARITY.	SIGNAL	1	21	
FT	DISUFDID	52	98	FT	CHAIN	22	BETA-LACTAMASE.
FT	BINDING	209	211	FT	ACT_SITE	66	BY SIMILARITY.
FT	SEQUENCE	265	AA;	FT	DISUFDID	73	BY SIMILARITY.
SEQUENCE	2860	MW;	B575CF3B1ADE304 CRC64;	FT	BINDING	230	SUBSTRATE (BY SIMILARITY).
QY				SQ	SEQUENCE	279	AA;
QY				SQ	SEQUENCE	30259	MW;
QY				SQ	SEQUENCE	CEC88E4B6BCDAEB	CRC64;
QY				Query Match			
QY				Best Local Similarity	67.3%		
QY				Score	905;	DB 1;	
QY				Length	279;		
QY				Best Local Similarity	66.7%		
QY				Score	929;	DB 1;	
QY				Length	265;		
QY				Best Local Similarity	67.6%		
QY				Pred. No.	1.4e-66;		
QY				Mismatches	38;		
QY				Indels	0;		
QY				Gaps	0;		
Db	2	PETLVKVDQDQGARVGYIELDNNGEELSERFPEMMSTPKVLLGAVSRIDA	61	QY	2	PETLVKVDQDQGARVGYIELDNNGEELSERFPEMMSTPKVLLGAVSRIDA	61
Db	2	PQPQEQIKLSSQLSGRGRVGMVEMDLASGRTRTAWRADERFMMSTPKVLLGAVSRIDA	61	Db	23	PQPQEQIKLSSQLSGRGRVGMVEMDLASGRTRTAWRADERFMMSTPKVLLGAVSRIDA	82
QY	62	GQBOLGRRIHVSQNDLVEYSVTEKHTDGMVRELSAATMSNTAANLILITIGGPK	121	QY	62	GQBOLGRRIHVSQNDLVEYSVTEKHTDGMVRELSAATMSNTAANLILITIGGPK	121
Db	62	GEDEQLERKIHQRQDLYDVSPEKSLHAGMVGELCAATMSDQAANLILATVGGA	121	Db	83	GEDEQLERKIHQRQDLYDVSPEKSLHAGMVGELCAATMSDQAANLILATVGGA	142
QY	122	ELTAFLHNNGDHTVRLDRMEPEANAEIPNDERDTTPVAMATTKLKIJTGELITLARQQ	181	QY	122	ELTAFLHNNGDHTVRLDRMEPEANAEIPNDERDTTPVAMATTKLKIJTGELITLARQQ	181
Db	122	GLTAFLRQIGDNTVRLDRMEPEANAEIPNDERDTTPVAMATTKLKIJTGELITLARQQ	202	Db	143	GLTAFLRQIGDNTVRLDRMEPEANAEIPNDERDTTPVAMATTKLKIJTGELITLARQQ	202
QY	182	LIDWMEADKVAGPLRSALPGWFLADKSGAGERSRGIIAALGPGKPSIIVWYTGS	241	QY	182	LIDWMEADKVAGPLRSALPGWFLADKSGAGERSRGIIAALGPGKPSIIVWYTGS	241
Db	182	LIDQWMDVDRVAGPLRSVLPAGMFLADKIGASKRGARGIVALIGPNKAERIVVYLDT	241	Db			



RESULT 13

BLAC_PROMI	STANDARD;	PRT;	298 AA.
ID P30897;			
DT 01-JUL-1993 (Rel. 26, Created)			
DT 01-JUL-1993 (Rel. 26, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Beta-lactamase precursor (EC 3.5.2.6) (Carbenicillinase).			
GN BLAP.			
OS Proteus mirabilis.			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC Enterobacteriaceae; Proteus.			
OX NCBI_TAXID=84;			
RN [1]			
RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-37.			
RC STRAIN=GN79;			
RX MEDLINE-9201595; PubMed=1840585;			
RA Sakurai Y., Tsukamoto K., Sawai T.;			
RT "Nucleotide sequence and characterization of a beta-lactamase gene from Proteus mirabilis."; J. Bacteriol. 173:7038-7041(1991).			
RT mirabilis.			
CC FUNCTION: Hydrolyzes carbenicillin.			
CC CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.			
CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.			
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CC EMBL; D13209; BAA02496.1; -.			
DR PIR; A41381; A41381.			
DR HSSP; P00810; ITEM.			
DR InterPro; IPR01466; Beta-lactamase.			
DR Pfam; PF00144; beta-lactamase.			
DR PRINTS; PRO0118; BLACTAMASE.			
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
KW Hydrolase; Antibiotic resistance; Signal.			
FT SIGNAL 1 28 POTENTIAL.			
FT CHAIN 29 298 BY SIMILARITY.			
FT ACT SITE 72 72 BY SIMILARITY.			
FT BINDING 237 239 SUBSTRATE (BY SIMILARITY).			
FT DISULFID 79 126 BY SIMILARITY.			
FT SEQUENCE 298 AA; 32765 MW; A3710008B728BD5F CRC64; 50.0% Score 672; DB 1; Length 298; Best Local Similarity 50.4%; Pred. No. 3.9e-46; Matches 130; Conservative 48; Mismatches 78; Indels 2; Gaps 2; OY 5 LIVKVKQAEADOLGARGVYIELDNLNGGETLESPRSEERPPMMTAKVILCGAVSIRIDAGE 64 152 TKEILRSIGDTTDLRMEPLNEAVPGDRTTPIAMVTTLEKLIDETISIKSROOLE 211			
Db 203 LQWQWUDDRVAGLRLSVPAGWTFIADKGAGRGARGIVALLGPNNKAERIVVILRDT 262 184 DMEDAKVAGLRLSVPAGWTFIADKGAGRGARGIVALLGPNNKAERIVVILRDT 241			
OY 242 QATMDERNRQIAQIAGASLIKW 263 212 SWIKGNIEVGDAIPLRKGVPSDWIVADRTGAGGGGSRAITAVMMWPNRKPITVAUYITDA 271			
Db 263 PASMAERNQOQIAGTAGALIEHW 284 244 TMDERNRQIAEIGASLIK 261 272 SFERNNAVIAKIGEQIAK 289			

RESULT 14

BLAC_AERY	STANDARD;	PRT;	304 AA.
ID BLAC_AERY			
DT 04-056; (Rel. 39, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last annotation update)			
DE Beta-lactamase AER-1 Precursor (EC 3.5.2.6) (Penicillinase).			
GN AER1.			
OS Aeromonas hydrophila.			
OC Aeromonadaceae; Aeromonas.			
OC NCBI_TAXID=64;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=YL7711; TRANSPONON=Omega7711;			
RX MEDLINE-9835319; PubMed=967391;			
RA Sauschadrin F., Bejaoui N., Levesque R.C.;			
RT "Structure of CARR-4 and AER-1 carbenicillin-hydrolyzing beta-lactamases.";			
RL Antimicrob. Agents Chemother. 42:1966-1972(1998).			
CC -!- FUNCTION: HYDROLYZES CARBENICILLIN. MECIICILLIN AND OXAICILLIN ARE WEAKLY HYDROLYZED.			
CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.			
CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.			
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CC EMBL; U14748; AAC0015.1; -.			
CC HSSP; P14557; ISHV			
CC InterPro; IPR01466; Beta-lactamase.			
CC DR InterPro; IPR000871; Beta-lactamase_A.			
CC DR InterPro; IPR000871; Beta-lactamase.			
CC DR Pfam; PF00144; beta-lactamase.			
CC DR PRINTS; PRO0118; BLACTAMASE.			
CC DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
CC DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
KW Hydrolase; Antibiotic resistance; Signal; Transposable element.			
FT SIGNAL 1 37 POTENTIAL.			
FT CHAIN 38 304 BY SIMILARITY.			
FT ACT SITE 83 83 BY SIMILARITY.			
FT DISTURD 90 137 POTENTIAL.			
FT BINDING 248 250 SUBSTRATE (BY SIMILARITY).			
FT SEQUENCE 304 AA; 3242 MW; 66AD56ED45D02A41 CRC64; 42.6% Score 573; DB 1; Length 304; Best Local Similarity 47.0%; Pred. No. 2.8e-38; Matches 119; Conservative 45; Mismatches 87; Indels 2; Gaps 2; OY 8 VDKAEDOLGARGVYIELDNLNGGETLESPRSEERPPMMTAKVILCGAVSIRIDAGE 67 47 VOSEESALHARVGMTFDSNIGITW-NYGRGDERFPINSTKTPSCAALLAKUDGKSLSIG 105			
Db 33 LEAVIATVETELGARIGAHDLTGKWE-HGSNERPLSSTFKL 91 65 QIGGRHYSQNDLVEISPVTEKHL-TDGMTRFLRCLRAITMDNTANLILITIGPKEL 123 92 RIDRVVRFSESSILVTPVTEKHVGKGMSLAECQATLSIDNSANFIQOQIGEPRAL 151 68 RRIYHSONDLYVEISPVTEKHL-TDGMTRFLRCLRAITMDNTANLILITIGPKELAF 126			

RESULT 15

BLC3\_PSEAE

ID BLC3\_PSEAE

STANDARD;

PRT: 288 AA.

AC P37322;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Beta-lactamase CARB-3 precursor (EC 3.5.2.6) (Carbenicillinase 3).

GN CARB3.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI\_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Cirole; TRANSPONSON=tn1408;

RX MEDLINE=91323732; PubMed=1650733;

RA Lachapelle J., Dufresne J., Levesque R.C.;

RT "Characterization of the blaCARB-3 gene encoding the carbenicillinase-3 beta-lactamase of *Pseudomonas aeruginosa*.";

RL Gene 102:7-12 (1991).

!-- FUNCTION: HYDROLYZES BOTH CARBENICILLIN AND OXACILLIN.

!-- CATALYTIC ACTIVITY: A beta-lactam + H<sub>2</sub>O = a substituted beta-amino acid.

!-- SIMILARITY: Belongs to the class-A beta-lactamase family.

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CC

DR EMBL; S46063; AAB19430.2; ALT\_INIT.

DR PIR; J01136; J01136.

DR HSSP; P14557; 15HV.

DR InterPro; IPR01466; Beta\_lactamase.

DR InterPro; IPR00871; Beta\_lactamase\_A.

DR Pfam; PF00144; beta\_lactamase\_1.

DR PRINTS; PRO0018; BLACTAMASE.

DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.

KW Hydrolase; Antibiotic\_resistance; Signal; Transposable\_element.

FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 1B 288 BETA-LACTAMASE CARB-3.

FT ACT\_SITE 65 65 BY SIMILARITY.

FT DISUFD 72 118 BY SIMILARITY.

FT BINDING 229 231 SUBSTRATE (BY SIMILARITY).

FT SEQUENCE 288 AA; 31313 MW; 38EBAR8789201AC6 CRC64;

Query Match 40.1%; Score 539.5; DB 1; Length 288;

Best Local Similarity 46.0%; Pred. No. 1.2e-35;

Matches 116; Conservative 42; Mismatches 93; Indels 1; Gaps 1;

QY 8 VKDAEOLGARGVGYEIDINSBILLESPRSEERFPPMMSTFKVILGAVISRIDAGQEQIG 67

29 VKAIELSLSRKIGVSYLDTQNGEYWD YNGNORFPLSTIFKTIACKALYDAQGKQVNP 87

QY 187 EADKVAGPLRSALPAGWFTADKSAGERSGRGSRGTAALGPGKPRIVWVITGQSOATMD 246

Db 226 LDQVAGALRASLFSDWKLTADKTAGGGYGSRSRIVAVIWPPSKQPLVVGIVYTQTKASMQ 285

QY 247 ERNQQIAEIGASL 259

Db 286 ASHQAAIARIGVWL 298

Search completed: June 18, 2004, 19:08:28  
Job time : 18 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 18, 2004, 18:59:13 ; Search time 21 Seconds  
(without alignments)

Sequence: 1 hpetlvkvkdaedqlgargv.....tndernrqiaeigaslikhw 263

Scoring table: BIOSIM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match Length	Query DB ID	Description
1	1330	98.9	286	S47061
2	1330	98.9	286	T51301
3	1330	98.9	286	S41975
4	1325	98.5	286	PNECP
5	1325	98.5	286	140905
6	1312	97.5	286	S60312
7	1311	97.5	286	S30113
8	1305	97.0	286	S60310
9	1303	96.9	286	S60311
10	1299	96.6	286	JQ1546
11	942	70.0	265	S00454
12	940	69.9	286	S16146
13	940	69.9	286	A60679
14	936	69.6	286	S02434
15	936	69.6	285	1 A44998
16	933	69.4	286	A37200
17	932	69.3	286	A60622
18	929	69.1	265	A60448
19	907.5	67.5	287	A44996
20	897	66.7	279	A24469
21	874	65.0	286	A44958
22	672	50.0	298	A41381
23	539.5	40.1	288	JQ1136
24	539.5	40.1	304	A35001
25	539.5	39.9	304	A49789
26	529.5	39.4	288	J50755
27	524.5	39.0	281	JG5395
28	39.0	10.5	276	JC2566
29	521	2.7	276	JH0268

RESULT 1

S47061

beta-lactamase (EC 3.5.2.6) - phage phi-X174

C;Species: phage phi-X174

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Jun-1999

C;Accession: S47061

R;Henrich, B.; Schmidtberger, B.

submitted to the EMBL Data Library, July 1994

A;Description: A variant of phix174 gene B-based positive selection vectors with enhanc

A;Reference number: S47060

A;Accession: S47061

A;Status: preliminary

A;Residues: 1-286 <HEN>

A;Cross-references: EMBL:Z35638; NID:9520995; PIDN:CAA84692.1; PID:9520998

C;Superfamily: beta-lactamase I

C;Keywords: hydrolase

Query Match 98.9%; Score 1330; DB 2; Length 286;

Best Local Similarity 98.9%; Pred. No. 3.5e-103; 1; Mismatches 2; Indels 0; Gaps 0;

Matches 260; Conservative 1; Description

QY

1 HPETLVKVDAEDQLGARGVYIELDINSGHLSFRSEERFPMMSSTKYLICGAVLSRID 60

Db

24 HPETLVKVDAEDQLGARGVYIELDINSGHLSFRSEERFPMMSSTKYLICGAVLSRID 83

QY

61 AGQSGLGRRHYSQNDLVYSPVYKHLTDGMVTRELSAATMSDNTANLJLITIGP 120

Db

84 AGQSGLGRRHYSQNDLVYSPVYKHLTDGMVTRELSAATMSDNTANLJLITIGP 143

QY

121 KELTAFLHNGDHTRLDRWEPPEINALPNDERTITPAMATIRKLTGELTASRQ 180

Db

144 KELTAFLHNGDHTRLDRWEPPEINALPNDERTITPAMATIRKLTGELTASRQ 203

QY

181 QLIDMEADKVGAPLRSALPAWFTADKSGAGGRGSGTIAALGPDKPSRITVWYITG 240

Db

204 QLIDMEADKVGAPLRSALPAWFTADKSGAGGRGSGTIAALGPDKPSRITVWYITG 263

QY

241 SQATMDERNRQIAIGASLIKHW 263

Db

264 SQATMDERNRQIAIGASLIKHW 286

RESULT 2

T51301

beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000

C;Accession: T51301

R;WACH, A.; BRACH, A.; ALBERTISEGU, C.; REBISCHUNG, C.; PHILIPPE, P.

A;Title: Heterologous HIS3 marker and GFP reporter module for pcp-targeting in Sacccharomyces pombe



A;Cross-references: EMBL:X65254; NID:9296955; PIDN:CA46346.1; PID:9296956  
 C;Superfamily: beta-lactamase I  
 Query Match 97.5%; Score 1312; DB 2; Length 286;  
 Best Local Similarity 97.0%; Pred. No. 1.1e-101; I  
 Matches 235; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 C;Accession: S60312  
 Db 181 QLIDWMEDKVAGPLRSALPAGWFLADKSGAGERSGRSGRTIAALGPDGKPSRIVIYTG 240  
 Db 204 QLIDWMEDKVAGPLRSALPAGWFLADKSGAGERSGRSGRTIAALGPDGKPSRIVIYTG 263  
 QY 241 SQATMDERNQIAEIGASLIKHW 263  
 Db 264 SQATMDERNQIAEIGASLIKHW 286

RESULT 5  
 140905 beta-lactamase (EC 3.5.2.6) - synthetic  
 C;Species: Synthetic  
 C;Note: cloning vector pCG1408 engineered and expressed in *Clavibacter xili* subsp. *cynod*  
 C;Date: 15-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Oct-2000  
 C;Accession: 140905  
 R;Taylor, J.; Stearman, R.S.; Urattani, B.B.  
 Plasmid 29, 241-244, 1993  
 A;Title: Development of a native plasmid as a cloning vector in *Clavibacter xili* subsp.  
 A;Reference number: 140904; MUID:93361581; PMID:7689234  
 A;Accession: 140905  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-286 <RES>  
 A;Cross-references: EMBL:U21228; NID:9885956; PIDN:AAA70411.1; PID:9885958  
 C;Keywords: hydrolase

Query Match 98.5%; Score 1325; DB 4; Length 286;  
 Best Local Similarity 98.1%; Pred. No. 9.1e-103;  
 Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 C;Accession: S60312  
 Db 1 HPETLVKVKDAEOLGARGVYIELDLNSGELESFRSERFPMSFKVLLGAVLSRID 60  
 Db 24 HPETLVKVKDAEOLGARGVYIELDLNSGKILLESFRERFPMSFKVLLGAVLSRID 83

QY 61 AGQEOLGRRIHYSQNDLVEYSPVTEKHLTDGMVTRELCSAITSMSDTAANLLITGGP 120  
 84 AGQEOLGRRIHYSQNDLVEYSPVTEKHLTDGMVTRELCSAITSMSDTAANLLITGGP 143  
 Db 121 KELTAFLHNGDVTDRWEPINEAPNDERDTTPVAMATTLKLTGELTLLASRQ 180  
 QY 144 KELTAFLHNGDVTDRWEPINEAPNDERDTTPVAMATTLKLTGELTLLASRQ 203  
 Db 181 QLIDWMEDKVAGPLRSALPAGWFLADKSGAGERSGRSGRTIAALGPDGKPSRIVIYTG 240  
 Db 204 QLIDWMEDKVAGPLRSALPAGWFLADKSGAGERSGRSGRTIAALGPDGKPSRIVIYTG 263  
 QY 241 SQATMDERNQIAEIGASLIKHW 263  
 Db 264 SQATMDERNQIAEIGASLIKHW 286

RESULT 6  
 S60312 extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*  
 C;Species: *Klebsiella pneumoniae*  
 C;Date: 12-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 22-Jun-1999  
 C;Accession: S60312  
 R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.  
 Antimicrob Agents Chemother, 36, 1817-1820, 1992  
 A;Title: Nucleotide sequences of CAZ-2, CAZ-5, and CAZ-7 beta-lactamase genes.  
 A;Reference number: S60310; MUID:93037315; PMID:1416873  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-286 <MB>  
 A;Cross-references: EMBL:X64523; NID:943797; PIDN:CAA45828.1; PID:943798  
 A;Gene: bla(TEM-3)  
 A;Genome: Plasmid  
 C;Superfamily: beta-lactamase I  
 C;Keywords: antibiotic resistance; hydrolase

Query Match 97.5%; Score 1311; DB 2; Length 286;  
 Best Local Similarity 97.0%; Pred. No. 1.3e-101; I  
 Matches 255; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 C;Accession: S60312  
 Db 1 HPETLVKVKDAEOLGARGVYIELDLNSGELESFRSERFPMSFKVLLGAVLSRID 60  
 Db 24 HPETLVKVKDAEOLGARGVYIELDLNSGKILLESFRERFPMSFKVLLGAVLSRID 83

QY 61 AGQEOLGRRIHYSQNDLVEYSPVTEKHLTDGMVTRELCSAITSMSDTAANLLITGGP 120  
 84 AGQEOLGRRIHYSQNDLVEYSPVTEKHLTDGMVTRELCSAITSMSDTAANLLITGGP 143  
 Db 121 KELTAFLHNGDVTDRWEPINEAPNDERDTTPVAMATTLKLTGELTLLASRQ 180  
 Db 144 KELTAFLHNGDVTDRWEPINEAPNDERDTTPVAMATTLKLTGELTLLASRQ 203  
 QY 181 QLIDWMEDKVAGPLRSALPAGWFLADKSGAGERSGRSGRTIAALGPDGKPSRIVIYTG 240  
 Db 204 QLIDWMEDKVAGPLRSALPAGWFLADKSGAGERSGRSGRTIAALGPDGKPSRIVIYTG 263  
 QY 241 SQATMDERNQIAEIGASLIKHW 263  
 Db 264 SQATMDERNQIAEIGASLIKHW 286

RESULT 6  
 S60312 residues: 1-286 <CBA>

RESULT 8		Matches
S60310	extended spectrum beta-lactamase CAZ-2 - <i>Klebsiella pneumoniae</i>	
C;Species: <i>Klebsiella pneumoniae</i>		
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999		
C;Accession: S60310		
R;Charal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.		
R;Antimicrob. Agents Chemother. 36: 1817-1820, 1992		
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.		
A;Reference number: S60310; MUID:93037315; PMID:1416873		
A;Accession: S60310		
A;Status: preliminary; translation not shown		
A;Molecule type: DNA		
A;Residues: 1-286 <CHA>		
A;Cross-references: EMBL:X65252; NID:9296951; PIDN:CAA46344.1; PID:g296952		
C;Superfamily: beta-lactamase I		
Query Match	97.0%; Score 1305; DB 2; Length 286;	
Best Local Similarity	96.6%; Pred. No. 4.2e-101; 4; Mismatches 5; Indels 0; Gaps 0;	
Matches 254;		
QY 1 HPETLVVKVDAEDQIGARVGYIELDNSCBLLESFRSERFPMMSTFKVLLCGAVLSRID 60		
Db 24 HPETLVVKVDAEDQIGARVGYIELDNSCBLLESFRSERFPMMSTFKVLLCGAVLSRID 83		
QY 61 AGQBOLGRRIHYSQNDLVKYSVPETEKHLTDGMVRELSAATMSDNTAANLLTTIGP 120		
Db 84 AGQBOLGRRIHYSQNDLVKYSVPETEKHLTDGMVRELSAATMSDNTAANLLTTIGP 143		
QY 121 KELTAFLHNGDHYTLDRWPEPELNEATPNDERDTTPAMATTKLTGELTLASRQ 180		
Db 144 KELTAFLHNGDHYTLDRWPEPELNEATPNDERDTTPAMATTKLTGELTLASRQ 203		
QY 181 QLIDWNEADKVAGPLRLSALPAGFIAIDKSGAGGERGSRGTAIALGPDKPSRIVIYTG 240		
Db 204 QLIDWNEADKVAGPLRLSALPAGFIAIDKSGAGGERGSRGTAIALGPDKPSRIVIYTG 263		
QY 241 SQATMDERNRQIAEIGASLIKHW 263		
Db 264 SQATMDERNRQIAEIGASLIKHW 286		
RESULT 9		
S60311	beta-lactamase (EC 3.5.2.6) TEM-1 - <i>Klebsiella pneumoniae</i> transposon Tn1331	
C;Species: <i>Klebsiella pneumoniae</i>		
C;Accession: S60311; F37392; PQ0498		
R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.		
R;Antimicrob. Agents Chemother. 36: 1817-1820, 1992		
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.		
A;Reference number: S60310; MUID:93037315; PMID:1416873		
A;Accession: S60311		
A;Status: preliminary; translation not shown		
A;Molecule type: DNA		
A;Residues: 1-286 <CAN>		
C;Genetics:		
A;Genome: plasmid		
C;Superfamily: beta-lactamase I		
Query Match	96.6%; Score 1299; DB 2; Length 286;	
Best Local Similarity	96.6%; Pred. No. 1.3e-100; 2; Mismatches 7; Indels 0; Gaps 0;	
Matches 254;		
QY 1 HPETLVVKVDAEDQIGARVGYIELDNSCBLLESFRSERFPMMSTFKVLLCGAVLSRID 60		
Db 24 HPETLVVKVDAEDQIGARVGYIELDNSCBLLESFRSERFPMMSTFKVLLCGAVLSRID 83		
QY 61 AGQBOLGRRIHYSQNDLVKYSVPETEKHLTDGMVRELSAATMSDNTAANLLTTIGP 120		
Db 84 AGQBOLGRRIHYSQNDLVKYSVPETEKHLTDGMVRELSAATMSDNTAANLLTTIGP 143		
QY 121 KELTAFLHNGDHYTLDRWPEPELNEATPNDERDTTPAMATTKLTGELTLASRQ 180		
Db 144 KELTAFLHNGDHYTLDRWPEPELNEATPNDERDTTPAMATTKLTGELTLASRQ 203		
QY 181 QLIDWNEADKVAGPLRLSALPAGFIAIDKSGAGGERGSRGTAIALGPDKPSRIVIYTG 240		
Db 204 QLIDWNEADKVAGPLRLSALPAGFIAIDKSGAGGERGSRGTAIALGPDKPSRIVIYTG 263		
QY 241 SQATMDERNRQIAEIGASLIKHW 263		
Db 264 SQATMDERNRQIAEIGASLIKHW 286		
RESULT 10		
S60311	Bla protein - <i>Salmonella typhimurium</i> plasmid NTP16	
N;Alternate names: beta-lactamase homolog		
C;Species: <i>Salmonella typhimurium</i>		
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999		
C;Accession: JO1546		
R;Cannon, P.M.; Strike, P.		
R;Plasmid 27, 220-230, 1992		
A;Title: Complete nucleotide sequence and gene organization of plasmid NTP16.		
A;Reference number: JO1538; MUID:92383313; PMID:1325061		
A;Accession: JO1546		
A;Status: translation not shown		
A;Molecule type: DNA		
A;Residues: 1-286 <CAN>		
C;Genetics:		
A;Genome: plasmid		
C;Superfamily: beta-lactamase I		
Query Match	96.6%; Score 1299; DB 2; Length 286;	
Best Local Similarity	96.6%; Pred. No. 1.3e-100; 2; Mismatches 7; Indels 0; Gaps 0;	
Matches 254;		
QY 1 HPETLVVKVDAEDQIGARVGYIELDNSCBLLESFRSERFPMMSTFKVLLCGAVLSRID 60		
Db 24 HPETLVVKVDAEDQIGARVGYIELDNSCBLLESFRSERFPMMSTFKVLLCGAVLSRID 83		
QY 61 AGQBOLGRRIHYSQNDLVKYSVPETEKHLTDGMVRELSAATMSDNTAANLLTTIGP 120		
Db 84 AGQBOLGRRIHYSQNDLVKYSVPETEKHLTDGMVRELSAATMSDNTAANLLTTIGP 143		
QY 121 KELTAFLHNGDHYTLDRWPEPELNEATPNDERDTTPAMATTKLTGELTLASRQ 180		
Db 144 KELTAFLHNGDHYTLDRWPEPELNEATPNDERDTTPAMATTKLTGELTLASRQ 203		
QY 181 QLIDWNEADKVAGPLRLSALPAGFIAIDKSGAGGERGSRGTAIALGPDKPSRIVIYTG 240		
Db 204 QLIDWNEADKVAGPLRLSALPAGFIAIDKSGAGGERGSRGTAIALGPDKPSRIVIYTG 263		
QY 241 SQATMDERNRQIAEIGASLIKHW 263		
Db 264 SQATMDERNRQIAEIGASLIKHW 286		
RESULT 11		
S00454	beta-lactamase (EC 3.5.2.6) class A - <i>Escherichia coli</i> plasmid p453	
N;Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1		
C;Species: <i>Escherichia coli</i>		
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993		
Query Match	96.9%; Score 1303; DB 2; Length 286;	
Best Local Similarity	96.2%; Pred. No. 6.1e-101;	

C:Accession: S00464  
 R;Barthelemy, M.; Peduzzi, J.; Labia, R.  
 Biochem. J. 251, 73-79, 1988  
 A;Title: Complete amino acid sequence of p453-plasmid-mediated PIR-2 beta-lactamase (SHV-2)  
 A;Reference number: S00464; MUID:88268817; PMID:3260490  
 A;Accession: S00464  
 A;Molecule type: protein  
 A;Residues: 1-265 <BAR>  
 C;Genetics:  
 C;Superfamily: beta-lactamase I  
 C;Keywords: antibiotic resistance; hydrolase

Query Match 70.0%; Score 942; DB 2; Length 265;  
 Best Local Similarity 68.3%; Pred. No. 6.2e-71; Matches 179; Conservative 38; Mismatches 45; Indels 0; Gaps 0;

QY 2 PETLVVKVKAEDQGARVYIELDINGSGILESFRSERPFPMSTPKVILGAVLSRIDA 61  
 Db 2 PETLVVKVKAEDQGARVYIELDINGSGILESFRSERPFPMSTPKVILGAVLSRIDA 61  
 QY 62 GQEQLGRRTHYSQNDLVEVSPVTEKHLTDGMTRELCSAITSMSDNAAANLLITGGPK 121  
 Db 62 GQEQLGRRTHYSQNDLVEVSPVTEKHLTDGMTRELCSAITSMSDNAAANLLITGGPK 121  
 QY 62 GDEQLERKIHRYQDILVDSYSPVSKHLAGMTGELCAAAITMSDNAAANLLITGGPK 121  
 Db 62 GDEQLERKIHRYQDILVDSYSPVSKHLAGMTGELCAAAITMSDNAAANLLITGGPK 121  
 QY 122 ELTAFLHNGDHVRLDRWPELNEAIPNDRDTPYAMATTURKLTGELITASRQ 181  
 Db 122 ELTAFLHNGDHVRLDRWPELNEAIPNDRDTPYAMATTURKLTGELITASRQ 181  
 QY 182 LIDWMEADKVGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 241  
 Db 182 LIDWMEADKVGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 241  
 QY 242 QATMDERNRQIAETGASLIKHW 263  
 Db 242 QATMDERNRQIAETGASLIKHW 263  
 Db 242 PASHAERNQOQIAGIGALIEHW 263

RESULT 12

S16146 beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids  
 N;Alternate names: beta-lactamase SHV2A  
 C;Species: Klebsiella pneumoniae  
 C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 15-Oct-1999  
 C;Accession: S16146; A35395; S18767  
 R;Podbielski, A.; Schoenling, J.; Neizer, B.; Warnatz, K.; Leusch, H.G.  
 J. Gen. Microbiol. 137, 5635-578, 1991  
 A;Title: Molecular characterization of a new Plasmid-encoded SHV-type beta-lactamase (SHV-2)  
 A;Reference number: S16146; MUID:91237320; PMID:2033379  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-286 <POD>  
 A;Cross-references: EMBL:Y53817; NID:943795; PIDN:CAA37813.1; PID:943796  
 A;Experimental source: plasmid pZMP1  
 R;Lee, K.Y.; Hopkins, J.D.; Syvanen, M.  
 J. Bacteriol. 172, 3229-3326, 1990  
 A;Title: Direct involvement of IS26 in an antibiotic resistance operon.  
 A;Reference number: A35395; MUID:90264317; PMID:2160941  
 A;Accession: A35395  
 A;Molecule type: DNA  
 A;Residues: 1-30, 'L', 32-286 <LEB>  
 A;Cross-references: GB:X62115; NID:948988; PIDN:CAA44025.1; PID:948990  
 C;Genetics:  
 A;Gene: blaS2A  
 A;Genome: plasmid  
 C;Superfamily: beta-lactamase I  
 C;Keywords: antibiotic resistance; hydrolase

Query Match 69.9%; Score 940; DB 2; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 1e-70; Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVVKVKAEDQGARVYIELDINGSGILESFRSERPFPMSTPKVILGAVLSRIDA 61  
 Db 2 PETLVVKVKAEDQGARVYIELDINGSGILESFRSERPFPMSTPKVILGAVLSRIDA 61  
 QY 23 PQLPQIKQESQSLQSGRVMIEMDLASGRITLAWRADERPFPMSTPKVILGAVLSRIDA 82  
 Db 23 PQLPQIKQESQSLQSGRVMIEMDLASGRITLAWRADERPFPMSTPKVILGAVLSRIDA 82  
 QY 62 GQEQLGRRTHYSQNDLVEVSPVTEKHLTDGMTRELCSAITSMSDNAAANLLITGGPK 121  
 Db 62 GQEQLGRRTHYSQNDLVEVSPVTEKHLTDGMTRELCSAITSMSDNAAANLLITGGPK 121  
 QY 182 LIDWMEADKVGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 241  
 Db 182 LIDWMEADKVGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 241  
 QY 203 LLQWVMDRVLGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 262  
 Db 203 LLQWVMDRVLGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 262  
 QY 242 QATMDERNRQIAETGASLIKHW 263  
 Db 242 QATMDERNRQIAETGASLIKHW 263  
 Db 263 PASHAERNQOQIAGIGALIEHW 284

RESULT 13

A60679 beta-lactamase (EC 3.5.2.6) SHV-2 precursor - Salmonella typhimurium plasmid pHT1  
 C;Species: Salmonella typhimurium  
 C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 28-May-1999  
 C;Accession: A60679  
 R;Garbarig-Cheron, A.; Godard, V.; Labia, R.; Nicolas, J.C.  
 Antimicrob. Agents Chemother. 34, 1444-1446, 1990  
 A;Title: Nucleotide sequence of SHV-2 beta-lactamase gene.  
 A;Reference number: A60679; MUID:90351141; PMID:2201259  
 A;Accession: A60679  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-286 <BAR>  
 A;Cross-references: GB:L47119; NID:972890; PIDN:AA75015.1; PID:9972891  
 C;Genetics:  
 C;Superfamily: beta-lactamase I  
 C;Keywords: antibiotic resistance; hydrolase  
 F;1-21/Domain: signal sequence #status predicted <SIG>

Query Match 69.9%; Score 940; DB 2; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 1e-70; Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVVKVKAEDQGARVYIELDINGSGILESFRSERPFPMSTPKVILGAVLSRIDA 61  
 Db 2 PETLVVKVKAEDQGARVYIELDINGSGILESFRSERPFPMSTPKVILGAVLSRIDA 61  
 QY 23 PQLPQIKQESQSLQSGRVMIEMDLASGRITLAWRADERPFPMSTPKVILGAVLSRIDA 82  
 Db 23 PQLPQIKQESQSLQSGRVMIEMDLASGRITLAWRADERPFPMSTPKVILGAVLSRIDA 82  
 QY 62 GQEQLGRRTHYSQNDLVEVSPVTEKHLTDGMTRELCSAITSMSDNAAANLLITGGPK 121  
 Db 62 GQEQLGRRTHYSQNDLVEVSPVTEKHLTDGMTRELCSAITSMSDNAAANLLITGGPK 121  
 QY 182 LIDWMEADKVGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 241  
 Db 182 LIDWMEADKVGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 241  
 QY 203 LLQWVMDRVLGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 262  
 Db 203 LLQWVMDRVLGAPLRLSALPAGWTFADKGAGRGSGRGGTAAAGPDPGKPSRIVWITGS 262  
 QY 242 QATMDERNRQIAETGASLIKHW 263  
 Db 242 QATMDERNRQIAETGASLIKHW 263  
 Db 263 PASHAERNQOQIAGIGALIEHW 284

RESULT 14

S02434 beta-lactamase (EC 3.5.2.6) SHV-2 - Escherichia coli  
 C;Species: Escherichia coli  
 C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993

Query Match 69.6%; Score 936; DB 2; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 2.e-70;  
 Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 62 GQFOLGRHYSQNDLVEYSPVTEKHLTDGMRRELCSAITSMSDNATANLILITGPK 121  
 Db 83 GDEQLERKHYRQODLVDYSPVSBKHLAGMTYGECLAAITWSDNSANLILITVGGEA 142

A;Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydrolase  
 A;Reference number: S02434; MUID:88196385; PMID:3129309  
 A;Residues: 1-265 <BAR>  
 A;Molecule type: protein  
 C;Superfamily: beta-lactamase\_I  
 C;Keywords: antibiotic resistance; hydrolase

Query Match 69.6%; Score 936; DB 2; Length 265;  
 Best Local Similarity 67.9%; Pred. No. 2.e-70;  
 Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVVKYKQADQGLGARVGYIELDINSGEILESRSEERPMSTPKVULCGAVLRSIDA 61  
 Db 2 PQPQIKUSQSLSGRVEMIDASGLPDTA  
 QY 62 GQEQLGRHYSQNDLVEYSPVTEKHLTDGMRRELCSAITSMSDNATANLILITGPK 121  
 Db 62 GDEQLERKHYRQODLVDYSPVSBKHLAGMTYGECLAAITWSDNSANLILITVGGEA 121

QY 122 ELTATLHNMGDHVRLDRWPELNEAIPNDERDTTPVAMATTURKLLTGBLLTASRQ 181  
 Db 122 GLTAFLRQIGDNVRLDRWPELNEAIPNDERDTTPVAMATTURKLLTGBLLTASRQ 181

QY 182 LIDWNEADKVYAGPLRLSALPAGWFLADKSCAGERSRGRTIAALGDGKPSRIVWYITGS 241  
 Db 182 LIDQWVDDRYTAGPLRLSALPAGWFLADKSCAGERSRGRTIAALGDGKPSRIVWYITGS 241

QY 242 QATWDERNRQIAEGASLKHW 263  
 Db 242 QATWDERNRQIAEGASLKHW 263

QY 243 GLTAFLRQIGDNVRLDRWPELNEAIPNDERDTTPVAMATTURKLLTGBLLTASRQ 181  
 Db 243 GLTAFLRQIGDNVRLDRWPELNEAIPNDERDTTPVAMATTURKLLTGBLLTASRQ 181

QY 182 LIDWNEADKVYAGPLRLSALPAGWFLADKSCAGERSRGRTIAALGDGKPSRIVWYITGS 241  
 Db 182 LIDQWVDDRYTAGPLRLSALPAGWFLADKSCAGERSRGRTIAALGDGKPSRIVWYITGS 241

QY 262 PASMARNQOIQAGIGALIEHW 284  
 Db 263 PASMARNQOIQAGIGALIEHW 284

RESULT 15

A44998 beta-lactamase (EC 3.5.2.6) SHV-2 - Klebsiella ozaenae plasmid pBP60  
 C;Species: Klebsiella ozaenae  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A44998; S12703  
 R;Huletsky, A.; Couture, F.; Levesque, R.C.  
 Antimicrob. Agents Chemother. 34, 1725-1732, 1990  
 R;Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.  
 A;Reference number: A44998; MUID:9136192; PMID:2285285  
 A;Accession: A44998  
 A;Stratus: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-286 <HUL>  
 A;Cross-references: GB:MG5179; NID:9150488; PID:AAA25526.1; PID:9150489  
 R;Pobialek, A.; Melzer, B.  
 Nucleic Acids Res. 18, 4916, 1990  
 A;Reference number: S12703; MUID:90370479; PMID:2395654  
 A;Accession: S12703  
 A;Stratus: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-286 <POD>  
 A;Cross-references: EMBL:X53433; NID:943789; PID:CAA37524.1; PID:943790  
 C;Genetics:  
 A;Genome: plasmid  
 C;Superfamily: beta-lactamase\_I  
 C;Keywords: antibiotic resistance; hydrolase

Query Match 69.6%; Score 936; DB 1; Length 286;  
 Best Local Similarity 67.9%; Pred. No. 2.e-70;  
 Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVVKYKQADQGLGARVGYIELDINSGEILESRSEERPMSTPKVULCGAVLRSIDA 61  
 Db 23 PQPQIKUSQSLSGRVEMIDASGLPDTA  
 QY 23 PQPQIKUSQSLSGRVEMIDASGLPDTA  
 Db 23 PQPQIKUSQSLSGRVEMIDASGLPDTA

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: June 18, 2004, 19:09:08 ; Search time 49 Seconds  
(without alignments)

Title:	EPPEPR526106.PEP	1515.275 Million cell updates/sec
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Gapopp:	10.0 , Gapext	0.5
Searched:	1163542 seqs, 282313646 residues	
Total number of hits satisfying chosen parameters:	1163542	
Minimum DB seq length:	0	
Maximum DB seq length:	200000000	
Post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 45 summaries		
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	5: /cgn2_6/ptodata/2/pubpaa/US07_PUB_COMB.pep:*	
	6: /cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*	
	7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*	
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	10: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*	
	11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*	
	12: /cgn2_6/ptodata/2/pubpaa/US09_PUB_COMB.pep:*	
	13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*	
	14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*	
	15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*	
	16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_COMB.pep:*	
	17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_COMB.pep:*	
	18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
%		
Result No.	Score	Match Length DB ID
1	1330	98.9 263 12 US-10-668-778-2
2	1330	98.9 285 10 US-09-919-901-7
3	1330	98.9 285 10 US-09-919-901-14
4	1330	98.9 286 10 US-09-919-901-21
5	1330	98.9 286 12 US-09-837-306-354
6	1330	98.9 286 14 US-10-191-966-7
7	1330	98.9 286 14 US-10-191-966-14
8	1330	98.9 286 14 US-10-191-966-21
9	1330	98.9 286 15 US-10-191-966-52
10	1330	98.9 2307 10 US-09-919-901-2
11	1330	98.9 2307 10 US-09-919-901-9
12	1330	98.9 2307 10 US-09-919-901-16
13	1330	98.9 2307 14 US-10-191-966-2
14	1330	98.9 2307 14 US-10-191-966-9
15	1330	98.9 2307 14 US-10-191-966-16

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1	1330	98.9	263	12	US-10-668-778-2	Sequence 2, Apply
2	1330	98.9	286	10	US-09-919-901-7	Sequence 7, Apply
3	1330	98.9	286	10	US-09-919-901-14	Sequence 14, Apply
4	1330	98.9	286	10	US-09-919-901-21	Sequence 21, Apply
5	1330	98.9	286	12	US-09-919-901-354	Sequence 354, Apply
6	1330	98.9	286	14	US-10-191-966-7	Sequence 7, Apply
7	1330	98.9	286	14	US-10-191-966-14	Sequence 14, Apply
8	1330	98.9	286	14	US-10-191-966-21	Sequence 21, Apply
9	1330	98.9	286	15	US-10-045-674-523	Sequence 523, Apply
10	1330	98.9	2307	10	US-09-919-901-2	Sequence 2, Apply
11	1330	98.9	2307	10	US-09-919-901-9	Sequence 9, Apply
12	1330	98.9	2307	10	US-09-919-901-16	Sequence 16, Apply
13	1330	98.9	2307	14	US-10-191-966-2	Sequence 2, Apply
14	1330	98.9	2307	14	US-10-191-966-9	Sequence 9, Apply
15	1330	98.9	2307	14	US-10-191-966-16	Sequence 16, Apply

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Maximum Match 100%
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ALIGNMENTS

RESULT 1  
US-10-668-778-2  
; Sequence 2, Application US/10668778  
; Publication No. US2010040038317A1  
; GENERAL INFORMATION:  
; APPLICANT: Balint, Robert F.  
; APPLICANT: Her, Jeng-Hong  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Interaction-activated Proteins

CURRENT APPLICATION NUMBER: US/10/668,778  
CURRENT REFERENCE: 02/116-00/000US  
PRIORITY APPLICATION NUMBER: US/09/526,106  
PRIORITY FILING DATE: 2000-03-15  
PRIORITY APPLICATION NUMBER: US 60/124,339  
PRIORITY FILING DATE: 1999-03-15  
PRIORITY APPLICATION NUMBER: US 60/135,926  
PRIORITY FILING DATE: 1999-05-25  
PRIORITY APPLICATION NUMBER: US 60/175,968  
PRIORITY FILING DATE: 2000-01-13  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 263  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
OTHER INFORMATION: TEM-1 beta-lactamase  
US-10-668-778-2

Query Match 98.9%; Score 1330; DB 12;  
 Best Local Similarity 98.9%; Pred. No. 6.5e-129;  
 Matches 260; Conservative 1; Mismatches 2;

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Sequence 292, App  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 7, Appli  
Sequence 5, Appli  
Sequence 4, Appli  
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Sequence 6, Appli  
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Sequence 65, Appli  
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Sequence 2, Appli  
Sequence 3, Appli  
Sequence 28, Appli  
Sequence 175764, A  
Sequence 73015, A

QY 61 AGOEOLGRRTHYSONDLVEYSPVTEKHLTDGMTRELCSAITSMSDNTAANLLTTIGP 120  
 Db 61 AGOEOLGRRTHYSONDLVEYSPVTEKHLTDGMTRELCSAITSMSDNTAANLLTTIGP 120  
 QY 121 KELTAFLHNNGDHVRLDRWEPPELNEAIUNDERDTTPVAMATURKLKLTGELTLASRQ 180  
 Db 121 KELTAFLHNNGDHVRLDRWEPPELNEAIUNDERDTTPVAMATURKLKLTGELTLASRQ 180  
 QY 181 QLIDWMEADKVAGPLRSALPAGWITADSKSGAGERSGSRGITALGPDKPSRIVIYTG 240  
 Db 181 QLIDWMEADKVAGPLRSALPAGWITADSKSGAGERSGSRGITALGPDKPSRIVIYTG 240  
 QY 241 SQATMDERNRQAEIGASLIKHW 263  
 Db 241 SQATMDERNRQAEIGASLIKHW 263

RESULT 2

US-09-919-901-7

; Sequence 7, Application US/09919901

; Publication No. US20030082518A1

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patck, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; FILE REFERENCE: 0125-005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; PRIOR APPLICATION NUMBER: 09/263,933

; PRIOR FILING DATE: 1999-02-08

; PRIOR APPLICATION NUMBER: 09/129,611

; CURRENT FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 09/263,933

; PRIOR FILING DATE: 1999-02-08

; PRIOR APPLICATION NUMBER: 09/129,611

; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02

; SEQ ID NO: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 14

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: ;

; OTHER INFORMATION: ;

US-09-919-901-14

; Sequence 14, Application US/09919901

; Publication No. US20030082518A1

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patck, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; FILE REFERENCE: 0125-005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; PRIOR APPLICATION NUMBER: 09/263,933

; CURRENT FILING DATE: 2001-08-02

; SEQ ID NO: 3

; SOFTWARE: PatentIn Ver. 2.0

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: ;

; OTHER INFORMATION: ;

US-09-919-901-7

; Sequence 7, Application US/09919901

; Publication No. US20030082518A1

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patck, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; FILE REFERENCE: 0125-005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; PRIOR APPLICATION NUMBER: 09/263,933

; CURRENT FILING DATE: 2001-08-02

; SEQ ID NO: 3

; SOFTWARE: PatentIn Ver. 2.0

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: ;

; OTHER INFORMATION: ;

US-09-919-901-14

; Sequence 14, Application US/09919901

; Publication No. US20030082518A1

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patck, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; FILE REFERENCE: 0125-005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; PRIOR APPLICATION NUMBER: 09/263,933

; CURRENT FILING DATE: 1999-02-08

; SEQ ID NO: 3

; SOFTWARE: PatentIn Ver. 2.0

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: ;

; OTHER INFORMATION: ;

US-09-919-901-14

; Sequence 14, Application US/09919901

; Publication No. US20030082518A1

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 US-09-919-901-14  
 ; Sequence 14, Application US/09919901  
 ; Publication No. US20030082518A1



PRIOR FILING DATE: 1999-03-08  
 PRIOR APPLICATION NUMBER: 09/129,611  
 PRIOR FILING DATE: 1998-08-05  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 14  
 LENGTH: 286  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION :  
 US-10-191-966-14

Query Match 98.9%; Score 1330; DB 14; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
 Matches 260; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Other Information: ;

Qy 1 HPETLVKVKDAEDQIGARVGYIELDINGSLSERESFRSEERFPMSSTFKVILCAGAVLSRID 60  
 Db 24 HPETLVKVKDAEDQIGARVGYIELDINGSLSERESFRSEERFPMSSTFKVILCAGAVLSRID 83  
 Qy 61 AGQEQLGRRIHYSONDIVEYSPVTEKHLTDGMTRVLCSAITMSDNTAANLLITIGP 120  
 Db 84 AGQEQLGRRIHYSONDIVEYSPVTEKHLTDGMTRVLCSAITMSDNTAANLLITIGP 143  
 Qy 121 KELTAFLHNGDHVTRLDWPELNEAIPNEDDTTPVAMATTURKLTGELTLASRQ 180  
 Db 144 KELTAFLHNGDHVTRLDWPELNEAIPNEDDTTPVAMATTURKLTGELTLASRQ 203  
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 Qy 181 QLIDWMEADKAGPLRSALPAGWFADKSGAGERSRGRTIAIGPDGKPSRIVVYTG 240  
 Db 204 QLIDWMEADKAGPLRSALPAGWFADKSGAGERSRGRTIAIGPDGKPSRIVVYTG 263  
 Qy 241 SQATMDERNRQIAEGASLIKHW 263  
 Db 264 SQATMDERNRQIAEGASLIKHW 286

RESULT 9  
 US-10-045-674-523  
 Sequence 523; Application US/10045674  
 Publication No. US2003023233A1  
 GENERAL INFORMATION:  
 APPLICANT: LADNER, ROBERT C.  
 APPLICANT: COHEN, BOWARD H.  
 APPLICANT: NASTRI, HORACIO G.  
 APPLICANT: ROOKY, KRISTIN L.  
 APPLICANT: HOET, RENE  
 APPLICANT: HOGGENBOOM, HENDRICKS R. J. M  
 TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
 TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
 TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
 TITLE OF INVENTION: LIBRARIES  
 FILE REFERENCE: DYX/002 CIP2  
 CURRENT APPLICATION NUMBER: US/10/045,674  
 CURRENT FILING DATE: 2001-10-25  
 CURRENT APPLICATION NUMBER: 60/198,069  
 PRIOR FILING DATE: 2000-04-17  
 PRIOR APPLICATION NUMBER: 09/837,306  
 PRIOR FILING DATE: 2001-04-17  
 NUMBER OF SEQ ID NOS: 635  
 SEQ ID NO: 523  
 LENGTH: 286  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS  
 OTHER INFORMATION: protein sequence  
 US-10-045-674-523

Query Match 98.9%; Score 1330; DB 15; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Other Information: ;

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 Qy 241 SQATMDERNRQIAEGASLIKHW 263  
 Db 264 SQATMDERNRQIAEGASLIKHW 286

RESULT 8  
 US-10-191-966-21  
 Sequence 21; Application US/10191966  
 Publication No. US20030175692A1  
 GENERAL INFORMATION:  
 APPLICANT: Potts, Karen E.  
 APPLICANT: Jackson, Roberta L.  
 APPLICANT: Patrick, Amy K.  
 TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
 FILE REFERENCE: 0125-0002A  
 CURRENT APPLICATION NUMBER: US/10/191,966  
 CURRENT FILING DATE: 2002-07-10  
 PRIOR APPLICATION NUMBER: US/09/263,933  
 PRIOR FILING DATE: 1999-03-08  
 PRIOR APPLICATION NUMBER: 09/129,611  
 PRIOR FILING DATE: 1998-08-05  
 NUMBER OF SEQ ID NOS: 33  
 SEQ ID NO: 21  
 LENGTH: 286  
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 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS  
 OTHER INFORMATION: protein sequence  
 US-10-045-674-523

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 Db 204 QLIDWMEADKAGPLRSALPAGWFADKSGAGERSRGRTIAIGPDGKPSRIVVYTG 263  
 Qy 241 SQATMDERNRQIAEGASLIKHW 263  
 Db 264 SQATMDERNRQIAEGASLIKHW 286



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; Sequence 2, Application US/10191966  
; Publication No. US20030175692A1  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patrick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/10/191, 966  
; CURRENT FILING DATE: 2002-07-10  
; PRIORITY APPLICATION NUMBER: US/09/263, 933  
; PRIORITY FILING DATE: 1998-08-05  
; PRIORITY APPLICATION NUMBER: 09/129, 611  
; PRIORITY FILING DATE: 1998-08-05  
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Db 2285 SQATMDERNRQIAEIGASLIKW 2307  
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US-10-191-966-9  
; Sequence 9, Application US/10191966  
; Publication No. US20030175692A1  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patrick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/10/191, 966  
; CURRENT FILING DATE: 2002-07-10  
; PRIORITY APPLICATION NUMBER: US/09/263, 933  
; PRIORITY FILING DATE: 1998-08-05  
; PRIORITY APPLICATION NUMBER: 09/129, 611  
; PRIORITY FILING DATE: 1998-08-05  
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Best Local Similarity 98.9%; Pred. No. 1.5e-127; Indels 0; Gaps 0;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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 QY 61 AGQOLGRGRHYSONDLVEYSPVYKHLUTGMVREICSAITMSDNTAAANLITGGP 120  
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 QY 121 KELTAFLHMGDHTRDRWPELNEAPNDERDTTVAMATTIRKLTGEILTLASRQ 180  
 Db 2165 KELTAFLHMGDHTRDRWPELNEAPNDERDTTVAMATTIRKLTGEILTLASRQ 2224  
 QY 181 QLIDWMEADTKVAGPLRSALPAGMFIADKSGAGERGSRGITAALGPDKPSRIVVYTG 240  
 Db 2225 QLIDWMEADTKVAGPLRSALPAGMFIADKSGAGERGSRGITAALGPDKPSRIVVYTG 2284  
 QY 241 SQAMDEERNRQARIGASLKH 263  
 Db 2285 SQAMDEERNRQARIGASLKH 2307

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Perfect score: 1345

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Score

Query

Match

Length

DB

ID

Description

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Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

Sequence 6, Appli

Sequence 7, Appli

Sequence 8, Appli

Sequence 9, Appli

Sequence 10, Appli

Sequence 11, Appli

Sequence 12, Appli

Sequence 13, Appli

Sequence 14, Appli

Sequence 15, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 18, Appli

Sequence 19, Appli

Sequence 20, Appli

Sequence 21, Appli

Sequence 22, Appli

Sequence 23, Appli

Sequence 24, Appli

RESULT 1  
US-07-721-775A-2  
; Sequence 2, Application US/07721775A  
; Patent No. 5180666  
; GENERAL INFORMATION:  
; ;  
; APPLICANT: States, J. Christopher  
; ;  
; APPLICANT: Hines, Ronald N.  
; ;  
; APPLICANT: No. 5180666A, Raymond F.  
; ;  
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING  
; ;  
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL  
; ;  
; NUMBER OF SEQUENCES: 2  
; ;  
; CORRESPONDENCE ADDRESS:  
; ;  
; ADDRESSEE: Resing, Ettington, Barnard, Perry & Milton  
; ;  
; STREET: P.O. Box 4390  
; ;  
; CITY: Troy  
; ;  
; STATE: Michigan  
; ;  
; COUNTRY: U.S.A.  
; ;  
; ZIP: 48039  
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; MEDIUM TYPE: Floppy disk  
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; COMPUTER: IBM PC compatible  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; ;  
; SOFTWARE: Patent in Release #11.0, Version #1.25  
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; CURRENT APPLICATION DATA:  
; ;  
; APPLICATION NUMBER: US/07/721-775A  
; ;  
; FILING DATE: 19910627  
; ;  
; CLASSIFICATION: 435  
; ;  
; ATTORNEY/AGENT INFORMATION:  
; ;  
; NAME: Kohn, Kenneth I.  
; ;  
; REGISTRATION NUMBER: 30,955  
; ;  
; REFERENCE/DOCENT NUMBER: P-321WSU  
; ;  
; TELECOMMUNICATION INFORMATION:  
; ;  
; TELEPHONE: (313) 689-3554  
; ;  
; TELEFAX: (313) 689-4071  
; ;  
; INFORMATION FOR SEQ ID NO: 2:  
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; SEQUENCE CHARACTERISTICS:  
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; TYPE: AMINO ACID  
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; TOPOLOGY: Linear  
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; MOLECULAR TYPE: protein

### ALIGNMENTS

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
Matches 260; Conservative 1; Mismatches 0; Gaps 0;  
Qy 1 HPTETVKVDAEDQLGARGVTEILDINGELESRSSEERPPMMSTKVLICGAVLSRID 60  
Db 24 HPTETVKVDAEDQLGARGVTEILDINGELESRSSEERPPMMSTKVLICGAVLSRID 83

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29 1325 98.5 285 4 Sequence 4, Appli  
30 1320 98.1 290 4 Sequence 4, Appli  
31 1318 98.0 265 2 Sequence 11407, A  
32 1318 98.0 265 2 Sequence 6, Appli  
33 1318 98.0 265 4 Sequence 6, Appli  
34 1317 97.9 264 2 Sequence 6, Appli  
35 1317 97.9 264 3 Sequence 8, Appli  
36 1317 97.9 264 4 Sequence 8, Appli  
37 1310.5 97.4 262 4 Sequence 3, Appli  
38 1310.5 97.4 262 4 Sequence 3, Appli  
39 1310.5 97.4 262 4 Sequence 3, Appli  
40 1308 97.2 286 1 US-08-346-333-16  
41 1308 97.2 285 4 PCT-US91-0506-16  
42 942 70.0 313 4 US-99-489-039A-11425  
43 499 37.1 142 4 US-09-489-039A-9803  
44 446 33.2 247 4 US-09-489-039A-11509  
45 441 32.8 192 4 US-09-489-039A-9460  
Sequence 16, Appli  
Sequence 16, Appli  
Sequence 11425, A  
Sequence 9803, Ap  
Sequence 11509, A  
Sequence 9460, Ap

RESULT 2  
US-08-339-658-2

Sequence 2, Application US/08339658  
; Sequence 2, Application US/08339658  
; Patent No. 552582

GENERAL INFORMATION:  
APPLICANT: States, J. Christopher  
APPLICANT: Hines, Ronald N.  
APPLICANT: No. 5525482K, Raymond F.  
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING  
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton  
STREET: P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
COUNTRY: U.S.A.  
ZIP: 48099

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/339,658  
FILING DATE: 15-NOV-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,295  
FILING DATE: 09-DEC-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Kohl, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-321MSU

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (313) 689-3554  
TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-339-658-2

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 3  
US-09-263-933-7

Sequence 7, Application US/09263933  
; Sequence 7, Application US/09263933  
; Patent No. 6280940

GENERAL INFORMATION:  
APPLICANT: Potts, Karen E.  
APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
FILE REFERENCE: 0125-005A

CURRENT APPLICATION NUMBER: US/09/263,933  
CURRENT FILING DATE: 1999-03-08  
EARLIER APPLICATION NUMBER: 091129,611  
EARLIER FILING DATE: 1998-08-05  
NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 286

TYPE: PRT  
ORGANISM: Artificial Sequence

US-09-263-933-7

Query Match 98.9%; Score 1330; DB 3; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 4  
US-09-263-933-14

Sequence 14, Application US/09263933  
; Sequence 14, Application US/09263933  
; Patent No. 6280940

GENERAL INFORMATION:  
APPLICANT: Potts, Karen E.  
APPLICANT: Jackson, Roberta L.  
APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
FILE REFERENCE: 0125-005A

QY 61 AGQEQGLGRRIHYSQNDLVEYSVTEKHLIDGTMVRELSAITSMSNTAANLLTIGGP 120  
Db 84 AGQEQGLGRRIHYSQNDLVEYSVTEKHLIDGTMVRELSAITSMSNTAANLLTIGGP 143  
QY 121 KELTAFLHNMGDHVTLDWPEPELNEATPENDERDTTPAMATIRKLIGELTLASRQ 180  
Db 144 KELTAFLHNMGDHVTLDWPEPELNEATPENDERDTTPAMATIRKLIGELTLASRQ 203  
QY 181 QLIDWMEAKVAGPLRSALPAGMFIADKSGAGERSGSGTIAALGPDGKPSRIVVYTG 240  
Db 204 QLIDWMEAKVAGPLRSALPAGMFIADKSGAGERSGSGTIAALGPDGKPSRIVVYTG 263  
QY 241 SQATMDERNRQIAELGASLKHW 263  
Db 264 SQATMDERNRQIAELGASLKHW 286

QY 121 KELTAFLHNMGDHVTLDWPEPELNEATPENDERDTTPAMATIRKLIGELTLASRQ 180  
Db 144 KELTAFLHNMGDHVTLDWPEPELNEATPENDERDTTPAMATIRKLIGELTLASRQ 203  
QY 181 QLIDWMEAKVAGPLRSALPAGMFIADKSGAGERSGSGTIAALGPDGKPSRIVVYTG 240  
Db 204 QLIDWMEAKVAGPLRSALPAGMFIADKSGAGERSGSGTIAALGPDGKPSRIVVYTG 263  
QY 241 SQATMDERNRQIAELGASLKHW 263  
Db 264 SQATMDERNRQIAELGASLKHW 286

QY 121 KELTAFLHNMGDHVTLDWPEPELNEATPENDERDTTPAMATIRKLIGELTLASRQ 180  
Db 144 KELTAFLHNMGDHVTLDWPEPELNEATPENDERDTTPAMATIRKLIGELTLASRQ 203  
QY 181 QLIDWMEAKVAGPLRSALPAGMFIADKSGAGERSGSGTIAALGPDGKPSRIVVYTG 240  
Db 204 QLIDWMEAKVAGPLRSALPAGMFIADKSGAGERSGSGTIAALGPDGKPSRIVVYTG 263  
QY 241 SQATMDERNRQIAELGASLKHW 263  
Db 264 SQATMDERNRQIAELGASLKHW 286

CURRENT APPLICATION NUMBER: US/09/263,933  
 CURRENT FILING DATE: 1999-03-08  
 EARLIER APPLICATION NUMBER: 09/129,611  
 EARLIER FILING DATE: 1998-08-05  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 14  
 LENGTH: 286  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 US-09-263-933-14

Query Match 98.9%; Score 1330; DB 3; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7..1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEDOLGARGVYIELDNSGETLESFRSEERFPMSFKVLLGAVLSRID 60  
 Db 24 HPETLVVKDAEDOLGARGVYIELDNSGETLESFRSEERFPMSFKVLLGAVLSRID 83  
 QY 61 AGOPOGLGRHRYSONDLYVEYSPVTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 120  
 Db 84 AGOPOGLGRHRYSONDLYVEYSPVTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 143  
 QY 121 KELTAFLHMGDVTRLDRWEPELINEAIPNDRDTTPVAMATTLRKLTGELTLASRQ 180

RESULT 5 US-09-025-769B-265  
 Sequence 265, Application US/09025769B  
 Patent No. 630064  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 ATTORNEY: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 TITLE OF INVENTION: Protein/ (Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 265:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 286 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-025-769B-265

RESULT 6 US-09-025-769B-265  
 Sequence 265, Application US/09025769B  
 Patent No. 630064  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 ATTORNEY: Pack, Peter  
 APPLICANT: Ilag, Vic  
 APPLICANT: Ge, Liming  
 APPLICANT: Moroney, Simon  
 TITLE OF INVENTION: Protein/ (Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 265:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 286 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-025-769B-265

Query Match 98.9%; Score 1330; DB 4; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7..1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEDOLGARGVYIELDNSGETLESFRSEERFPMSFKVLLGAVLSRID 60  
 Db 24 HPETLVVKDAEDOLGARGVYIELDNSGETLESFRSEERFPMSFKVLLGAVLSRID 83  
 QY 61 AGOPOGLGRHRYSONDLYVEYSPVTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 120  
 Db 84 AGOPOGLGRHRYSONDLYVEYSPVTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 143  
 QY 121 KELTAFLHMGDVTRLDRWEPELINEAIPNDRDTTPVAMATTLRKLTGELTLASRQ 180

Query Match 98.9%; Score 1330; DB 3; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7..1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEDOLGARGVYIELDNSGETLESFRSEERFPMSFKVLLGAVLSRID 60  
 Db 24 HPETLVVKDAEDOLGARGVYIELDNSGETLESFRSEERFPMSFKVLLGAVLSRID 83  
 QY 61 AGOPOGLGRHRYSONDLYVEYSPVTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 120  
 Db 84 AGOPOGLGRHRYSONDLYVEYSPVTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 143  
 QY 121 KELTAFLHMGDVTRLDRWEPELINEAIPNDRDTTPVAMATTLRKLTGELTLASRQ 180

RESULT 7  
US-09-025-769B-362  
Sequence 362, Application US/09025769B  
Patient No. 630064  
GENERAL INFORMATION:  
APPLICANT: Krappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Blueckhun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr. Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025, 769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9090  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 362:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-362

Query Match, Best Local Similarity 98.9%; Score 1330; DB 4; Length 286; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0; US-09-025-769B-362

Query 1 HPETLKVKDAEDQGARVYVTELDNSGETLESEPFKVLICGAVLRSID 60  
Db 24 HPETLKVKDAEDQGARVYVTELDNSGETLESEPFKVLICGAVLRSID 83  
Query 61 AGQEQLGRHYSQNDLVEYSPVTEKLTGMDTVERLCSAITSMSNTAANLLTTIGP 120  
Db 121 KELTAFLHNMGDHVTLDRPELNEAIRUDERDTTPVAMATLRLKGELLTASRQ 180  
Query 144 KELTAFLHNMGDHVTLDRPELNEAIRUDERDTTPVAMATLRLKGELLTASRQ 203  
Db 181 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSRGSGITIALGPDKPSRIVIYTG 240  
Db 204 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSRGSGITIALGPDKPSRIVIYTG 263  
Db 264 SQATMDERNRQIAEIGASLIKW 286

RESULT 8  
US-09-919-901-7  
Sequence 7, Application US/09919901  
Patient No. 6599738  
GENERAL INFORMATION:  
APPLICANT: Potts, Karen E.  
APPLICANT: Jackson, Roberta L.  
APPLICANT: Patrick, Amy K.  
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
FILE REFERENCE: 0125-005A  
CURRENT APPLICATION NUMBER: US/09/919, 901  
PRIORITY FILING DATE: 2001-08-02  
PRIORITY APPLICATION NUMBER: 09/163, 933  
PRIORITY FILING DATE: 1995-02-06  
PRIORITY APPLICATION NUMBER: 09/129, 611  
PRIORITY FILING DATE: 1998-08-05  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 286  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: :  
US-09-919-901-7

Query Match, Best Local Similarity 98.9%; Score 1330; DB 4; Length 286; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0; US-09-919-901-7

Query 1 HPETLKVKDAEDQGARVYVTELDNSGETLESEPFKVLICGAVLRSID 60  
Db 84 AGQEQLGRHYSQNDLVEYSPVTEKLTGMDTVERLCSAITSMSNTAANLLTTIGP 143  
Db 24 HPETLKVKDAEDQGARVYVTELDNSGETLESEPFKVLICGAVLRSID 83  
Query 121 KELTAFLHNMGDHVTLDRPELNEAIRUDERDTTPVAMATLRLKGELLTASRQ 180  
Db 144 KELTAFLHNMGDHVTLDRPELNEAIRUDERDTTPVAMATLRLKGELLTASRQ 203  
Query 181 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSRGSGITIALGPDKPSRIVIYTG 240  
Db 204 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSRGSGITIALGPDKPSRIVIYTG 263  
Db 264 SQATMDERNRQIAEIGASLIKW 286

RESULT 9  
US-09-919-901-14  
Sequence 14, Application US/09919901  
Patient No. 6599738  
GENERAL INFORMATION:  
APPLICANT: Potts, Karen E.  
APPLICANT: Jackson, Roberta L.  
APPLICANT: Patrick, Amy K.  
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
FILE REFERENCE: 0125-005A  
CURRENT APPLICATION NUMBER: US/09/919, 901  
CURRENT FILING DATE: 2001-08-02

Query 121 KELTAFLHNMGDHVTLDRPELNEAIRUDERDTTPVAMATLRLKGELLTASRQ 180  
Query 144 KELTAFLHNMGDHVTLDRPELNEAIRUDERDTTPVAMATLRLKGELLTASRQ 203  
Db 181 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSRGSGITIALGPDKPSRIVIYTG 240

; PRIOR APPLICATION NUMBER: 09/263, 933  
 ; PRIOR FILING DATE: 1999-02-08  
 ; PRIOR APPLICATION NUMBER: 09/129, 611  
 ; PRIOR FILING DATE: 1998-08-05  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 14  
 ; LENGTH: 286  
 ; TYPE: PR1  
 ; ORGANISM: Artificial Sequence  
 ; OTHER INFORMATION: :  
 ; US-09-919-901-14

Query Match 98.9%; Score 1330; DB 4; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 60  
 Db 24 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 83

Query Match 98.9%; Score 1330; DB 4; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 60  
 Db 24 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 83

RESULT 10  
 US-09-919-901-21

; Sequence 21, Application US/09919901  
 ; Patent No. 6599138

; GENERAL INFORMATION:  
 ; APPLICANT: Potts, Karen E.  
 ; APPLICANT: Jackson, Roberta L.  
 ; APPLICANT: Patrick, Amy K.  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; TITLE OF INVENTION: OP INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
 ; FILE REFERENCE: 012-9008A  
 ; CURRENT APPLICATION NUMBER: US/09/919, 901  
 ; CURRENT FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: 09/263, 933  
 ; PRIOR FILING DATE: 1999-02-08  
 ; PRIOR APPLICATION NUMBER: 09/129, 611  
 ; PRIOR FILING DATE: 1998-08-05  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 21  
 ; LENGTH: 286  
 ; TYPE: PR1  
 ; FEATURE: OTHER INFORMATION: :

; US-09-919-901-21

Query Match 98.9%; Score 1330; DB 4; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 60  
 Db 24 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 83

RESULT 11  
 US-09-025-769B-285

; Sequence 285, Application US/09025769B  
 ; Patent No. 6300064

; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Pack, Peter  
 ; APPLICANT: Ilag, Vic  
 ; APPLICANT: Ge, Liming  
 ; APPLICANT: Moroney, Simon  
 ; APPLICANT: Blueckthun, Andreas  
 ; TITLE OF INVENTION: Protein/(poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10021

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/025, 769B  
 ; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: James F. Haley, Jr., Esq.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212)596-9000  
 ; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 285:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 299 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

; US-09-025-769B-285

Query Match 98.9%; Score 1330; DB 4; Length 299;  
 Best Local Similarity 98.9%; Pred. No. 7.6e-139;  
 Matches 260; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 60  
 Db 24 HPETIVKVKDAEDQIGARVGYIELDINSGKILSFRPFERFPMSTFKVLCAVLSRID 83

; 61 AGEQQLGRRIHYSNDLVEYSPTKEHLDGMVTRELCSAALTMSDNTAANLLTTGGP 120  
 ; 84 AGEQQLGRRIHYSNDLVEYSPTKEHLDGMVTRELCSAALTMSDNTAANLLTTGGP 143  
 ; 121 KELTAFLHMGHVTDRWEPINEALPNDERTTTPVAMATTIRKULTGELTILASRQ 180  
 ; 144 KELTAFLHMGHVTDRWEPINEALPNDERTTTPVAMATTIRKULTGELTILASRQ 203  
 ; 181 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSGRGIAALGPDKPSRIVIYTG 240  
 ; 204 QLIDWMEADKVAGPLRSALPAGWFIAKSGAGERSGRGIAALGPDKPSRIVIYTG 263

RESULT 12  
US-99-025-769B-298

Sequence 298 Application US/09025769B

Patent No. 630064

GENERAL INFORMATION:

APPLICANT: Knapik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Blueckhun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient In Release #1.0, version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 298:

SEQUENCE CHARACTERISTICS:

LENGTH: 299 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-298

Query Match 98.9%; Score 1330; DB 4; Length 299;

Best Local Similarity 98.9%; Pred. No. 7.6e-139; Length 299;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKADOLGARYGYIELDINGSKLESPRSERFPRPFMSPTKVILGAVLSRID 60

QY 24 HPETLVKVKADOLGARYGYIELDINGSKLESPRSERFPRPFMSPTKVILGAVLSRID 83

QY 61 AGQBQGRRIHYSONDLVESPVTPKHLTGMTRRELCSAITSMSNTAANLLTTIGP 120

QY 84 AGQBQGRRIHYSONDLVESPVTPKHLTGMTRRELCSAITSMSNTAANLLTTIGP 143

Db 264 SQATMDERNRQIAEGASLIKW 286

RESULT 13  
US-09-025-769B-300

Sequence 300 Application US/09025769B

Patent No. 630064

GENERAL INFORMATION:

APPLICANT: Knapik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Blueckhun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 300:

SEQUENCE CHARACTERISTICS:

LENGTH: 299 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-300

Query Match 98.9%; Score 1330; DB 4; Length 299;

Best Local Similarity 98.9%; Pred. No. 7.6e-139; Length 299;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKADOLGARYGYIELDINGSKLESPRSERFPRPFMSPTKVILGAVLSRID 60

QY 24 HPETLVKVKADOLGARYGYIELDINGSKLESPRSERFPRPFMSPTKVILGAVLSRID 83

QY 61 AGQBQGRRIHYSONDLVESPVTPKHLTGMTRRELCSAITSMSNTAANLLTTIGP 120

QY 84 AGQBQGRRIHYSONDLVESPVTPKHLTGMTRRELCSAITSMSNTAANLLTTIGP 143

Db 121 KELTAFLHNINGDHDVTRLDREPELNEAIUNDERDTTPVAMATTURKLITGELTLASRQ 180

Db 144 KELTAFLHNINGDHDVTRLDREPELNEAIUNDERDTTPVAMATTURKLITGELTLASRQ 203

QY 181 QLIDWMEADKVGPLRSALPAGWFTADSKGAGERSGSRGTAALGPDGKPSRIVVYTG 240

Db 204 QLIDWMEADKVGPLRSALPAGWFTADSKGAGERSGSRGTAALGPDGKPSRIVVYTG 263

QY 241 SQATMDERNRQIAEGASLIKW 263

Db 264 SQATMDERNRQIAEGASLIKW 286

QY 121 KELTAFLHNINGDHDVTRLDREPELNEAIUNDERDTTPVAMATTURKLITGELTLASRQ 180

Db 144 KELTAFLHNINGDHDVTRLDREPELNEAIUNDERDTTPVAMATTURKLITGELTLASRQ 203

QY 181 QLIDWMEADKVGPLRSALPAGWFTADSKGAGERSGSRGTAALGPDGKPSRIVVYTG 240

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QY 241 SQATMDERNRQIAEGASLIKW 263

Db 264 SQATMDERNRQIAEGASLIKW 286

Db 144 KELTAFLHNMGDHVTRIDRWEPELNEAPNDERTTMVAMATTURKLTGELTLASRQ 203 ; EARLIER APPLICATION NUMBER: 091129, 611  
 QY 181 QLIDWMEDAKVAGPLRSALPAGWFIADKSGAGERSGRIAALGPDGKPSRIVIYTG 240 ; EARLIER FILING DATE: 1998-08-05  
 ; NUMBER OF SEQ ID NOS: 33  
 Db 204 QLIDWMEDAKVAGPLRSALPAGWFIADKSGAGERSGRIAALGPDGKPSRIVIYTG 263 ; SEQ ID NO: 9  
 ; LENGTH: 2307  
 ;  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263 ; TYPE: PRT  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286 ; ORGANISM: Artificial Sequence  
 ; US-09-263-933-9

Query Match 98.9%; Score 1330; DB 3; Length 2307;  
 Best Local Similarity 98.9%; Pred. No. 1.8e-137; Matches 260; Conservative 98.9%; 1; Mismatches 2; Indels 0; Gaps 0;  
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 Db 2045 HPETLVKVDAAEOLGARGVYIELDNSGEILSFRSERPFMSTPKVILCGAVLSRID 2104 ;  
 QY 61 AGQBOLGRRIHYSONDLVYSPTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 120 ;  
 Db 2105 AGQBOLGRRIHYSONDLVYSPTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 2164 ;  
 QY 121 KELTAFLHNMGDHVTRIDRWEPELNEAPNDERTTMVAMATTURKLTGELTLASRQ 180 ;  
 Db 2165 KELTAFLHNMGDHVTRIDRWEPELNEAPNDERTTMVAMATTURKLTGELTLASRQ 2224 ;  
 QY 181 QLIDWMEDAKVAGPLRSALPAGWFIADKSGAGERSGRIAALGPDGKPSRIVIYTG 240 ;  
 Db 2225 QLIDWMEDAKVAGPLRSALPAGWFIADKSGAGERSGRIAALGPDGKPSRIVIYTG 2284 ;  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263 ;  
 Db 2285 SQATMDERNRQIAEIGASLIKHW 2307 ;

RESULT 14  
 US-09-263-933-2  
 ; Sequence 2, Application US/09263933  
 ; Patent No. 6280940  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Potts, Karen E.  
 ; APPLICANT: Jackson, Roberta L.  
 ; APPLICANT: Patick, Amy K.  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; FILE REFERENCE: 0125-005A  
 ; CURRENT APPLICATION NUMBER: US/09/263, 933  
 ; CURRENT FILING DATE: 1999-03-08  
 ; EARLIER APPLICATION NUMBER: 09/129, 611  
 ; EARLIER FILING DATE: 1998-08-05  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SEQ ID NO: 9  
 ; LENGTH: 2307  
 ;  
 ; ORGANISM: Artificial Sequence  
 ; US-09-263-933-9

Query Match 98.9%; Score 1330; DB 3; Length 2307;  
 Best Local Similarity 98.9%; Pred. No. 1.8e-137; Matches 260; Conservative 98.9%; 1; Mismatches 2; Indels 0; Gaps 0;  
 Matches 260; Conservative 98.9%; Pred. No. 1.8e-137; Matches 260; Conservative 98.9%; 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HPETLVKVDAAEOLGARGVYIELDNSGEILSFRSERPFMSTPKVILCGAVLSRID 60 ;  
 Db 2045 HPETLVKVDAAEOLGARGVYIELDNSGEILSFRSERPFMSTPKVILCGAVLSRID 2104 ;  
 QY 61 AGQBOLGRRIHYSONDLVYSPTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 120 ;  
 Db 2105 AGQBOLGRRIHYSONDLVYSPTEKHLTDGMVRELSAATMSDNTAANLLTTGGP 2164 ;  
 QY 121 KELTAFLHNMGDHVTRIDRWEPELNEAPNDERTTMVAMATTURKLTGELTLASRQ 180 ;  
 Db 2165 KELTAFLHNMGDHVTRIDRWEPELNEAPNDERTTMVAMATTURKLTGELTLASRQ 2224 ;  
 QY 181 QLIDWMEDAKVAGPLRSALPAGWFIADKSGAGERSGRIAALGPDGKPSRIVIYTG 240 ;  
 Db 2225 QLIDWMEDAKVAGPLRSALPAGWFIADKSGAGERSGRIAALGPDGKPSRIVIYTG 2284 ;  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263 ;  
 Db 2285 SQATMDERNRQIAEIGASLIKHW 2307 ;

Search completed: June 18, 2004, 19:10:35  
 Job time : 23 secs

RESULT 15  
 US-09-263-933-9  
 ; Sequence 9, Application US/09263933  
 ; Patent No. 6280940  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Potts, Karen E.  
 ; APPLICANT: Jackson, Roberta L.  
 ; APPLICANT: Patick, Amy K.  
 ; APPLICANT: Jackson, Roberta L.  
 ; APPLICANT: Patick, Amy K.  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; FILE REFERENCE: 0125-005A  
 ; CURRENT APPLICATION NUMBER: US/09/263, 933  
 ; CURRENT FILING DATE: 1999-03-08

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OM protein - protein search, using sw model

Run on:

June 18, 2004, 19:01:08 ; Search time 45 Seconds

(without alignments)

1844.029 Million cell updates/sec

Title: EPPER526106.PEP

Perfect score: 1345

Sequence: hptelvkvdaedqlgarvg.....tdemrrqiaeigaslikhw 263

Scoring table: BLOSUM2

Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL\_25:\*

- 1: SP\_archaea:\*
- 2: SP\_bacteria:\*
- 3: SP\_fungi:\*
- 4: SP\_invertebrates:\*
- 5: SP\_mammal:\*
- 6: SP\_mhc:\*
- 8: SP\_organelle:\*
- 9: SP\_phage:\*
- 10: SP\_plant:\*
- 11: SP\_insect:\*
- 12: SP\_virus:\*
- 13: SP\_vertebrate:\*
- 14: SP\_unclassified:\*
- 15: SP\_rvirus:\*
- 16: SP\_bacteriapl:\*
- 17: SP\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 2 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 3 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 4 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 5 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 6 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 7 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 8 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 9 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 10 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 11 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-1995 (TRIMBLrel. 01, last sequence update)

DT 01-JUN-2003 (TRIMBLrel. 24, last annotation update)

DE Beta-lactamase precursor (EC 3.5.2.6) (penicillinase).

GN BUL OR AMPR.

SP Staphylococcus aureus,

OS Escherichia coli,

OS unidentified, and

OS Alcaligenes hydrogenophilus.

OG Plasmid pJD884, plasmid pRP4 and plasmid pRAY-1.

OC Bacteria; Firmicutes; Bactillales; Staphylococcus.

NCBI\_TAXID=1280, 562, 32644, 516;

[1]

RESULT 12 ID Q00626 PRELIMINARY; PRT; 286 AA.

AC Q00626; Q57339; Q08022; Q081102; Q09490; Q09483; Q09393; Q09396;

AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;

AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;

DT 01-NOV-199

RT "Two new members of the bio B superfamily: cloning, sequencing and expression of bio B genes of *Methylobacillus flagellatum* and *Corynebacterium glutamicum*.";  
 RT Gene 175:15-22(1996).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R12;  
 RA Rondot S., Anthony K., Dubel S., Ida N., Bayreuther K., Frost L.,  
 RA Little M., Breitling F.,  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9636236; PubMed=8770413;  
 RA Rees S., Cote J., Stables J., Harris S., Lee M.G.,  
 RT "Bicistronic vector for the creation of stable mammalian cell lines that predisposes all antibiotic-resistant cells to express recombinant protein.";  
 RT Biotechniques 20:102-104(1995).  
 RL [8]  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97105907; PubMed=8948655;  
 RA Storch T., Krueh U., Kolhekar R., Sprengel R., Seeburg P.H.;  
 RT "rapid construction in yeast of complex targeting vectors for gene manipulation in the mouse.";  
 RL Nucleic Acids Res. 24:4594-4596(1996).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RX SEQUENCE FROM N.A.  
 RA Lou Q.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RA Holtz A., Lou Y.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92332280; PubMed=1319065;  
 RA Gossen M., Bujard H.,  
 RT "right control of gene expression in mammalian cells by tetracycline-responsive promoters.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551(1992).  
 RL [13]  
 RP SEQUENCE FROM N.A.  
 RA Gossen M., Bujard H.,  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
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 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96032859; PubMed=7567477;  
 RA Baron U., Freundlieb S., Gossen M., Bujard H.;  
 RT "Co-regulation of two gene activities by tetracycline via a bidirectional promoter";  
 RL Nucleic Acids Res. 23:3605-3606(1995).  
 RN [16]  
 RP SEQUENCE FROM N.A.  
 RA Baron U., Freundlieb S., Gossen M., Bujard H.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
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 RA Kitts P.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [18]  
 RP SEQUENCE FROM N.A.  
 RA Schleper D., von Wilcken-Bergmann B., Schmidt M., Sobek H.,  
 RA Mueller-Hill B.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-

CC AMINO ACID.  
 CC -1- SIMILARITY: THIS IS A CLASS-A BETA-LACTAMASE.  
 CC DR EMBL; U36912; AAB39957.1; -.  
 CC DR EMBL; M7750; AAB24057.1; -.  
 CC DR EMBL; U36911; AAB39956.1; -.  
 CC DR EMBL; U31280; AAC44581.1; -.  
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 CC DR EMBL; U89932; AAB64392.1; -.  
 CC DR EMBL; U89933; AAB64394.1; -.  
 CC DR EMBL; U89934; AAB64395.1; -.  
 CC DR EMBL; U89935; AAB64398.1; -.  
 CC DR EMBL; U89937; AAB64401.1; -.  
 CC DR EMBL; U89938; AAB64403.1; -.  
 CC DR EMBL; U89939; AAB64405.1; -.  
 CC DR EMBL; U89940; AAB64407.1; -.  
 CC DR EMBL; U89671; AAB9977.1; -.  
 CC DR GO; GO:004681; C-extrachromosomal DNA; IEA.  
 CC DR GO; GO:0008800; F-beta-Lactamase activity; IEA.  
 CC DR GO; GO:0016787; F-hydrolase activity; IEA.  
 CC DR GO; GO:004677; Proline kinase activity; IEA.  
 CC DR InterPro; IPR01466; Beta-Lactamase.  
 CC DR InterPro; IPR00081; Beta-Lactamase\_A.  
 CC DR Pfam; PF00144; beta-Lactamase; 1.  
 CC DR PRINTS; PR0018; BLACTAMASE.  
 CC DR PROSITE; PS00146; BETA-LACTAMASE\_A; 1.  
 CC KW Antibiotic resistance; Hydrolase; Plasmid; Signal.  
 CC FT SIGNAL 1 23  
 CC FT CHAIN 24 286 BETA-LACTAMASE II.  
 CC FT SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;  
 CC  
 Query Match 98.9%; Score 1330; DB 2; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 4.3e-104;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 HPETLVKQDAEDOLGARYGIVELDINSCTLESFRPSRERFPMSITPKVLLCGAVSRID 60  
 Db 24 HPETLVKQDAEDOLGARYGIVELDINSCTLESFRPSRERFPMSITPKVLLCGAVSRID 83  
 Qy 61 AGQEQLGRGRHYSQDLYEVSPVTEKHLIDGMTRFLRELCASAITMSDNTAANLLTIGP 120  
 Db 84 AGQEQLGRGRHYSQDLYEVSPVTEKHLIDGMTRFLRELCASAITMSDNTAANLLTIGP 143  
 Qy 121 KELTAFLHNNGDHVTRLDRMPELNEAIPENDRTTPVAMTLLRKLGELITLARO 180  
 Db 144 KELTAFLHNNGDHVTRLDRMPELNEAIPENDRTTPVAMTLLRKLGELITLARO 203  
 Qy 181 QLIDWMAEKVAGPLSLAPAGWETADSKSAGERSGRGSGTIALGPDGKPSRIVWYTG 240  
 Db 204 QLIDWMAEKVAGPLSLAPAGWETADSKSAGERSGRGSGTIALGPDGKPSRIVWYTG 263  
 Qy 241 SQATMDERNROIAEIGASLKHW 263  
 Db 264 SQATMDERNROIAEIGASLKHW 266  
 CC RESULT 2  
 CC ID Q38058 PRELIMINARY; PRT; 286 AA.  
 CC AC 038058  
 CC DT 01-NOV-1995 (T-EMBLrel. 01, Created)  
 CC DT 01-NOV-1996 (T-EMBLrel. 01, last sequence update)  
 CC DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)  
 CC DR Beta-lactamase.  
 CC BLA.





Query Match, 98.2%; Score 1321; DB 2; Length 286;  
 Best Local Similarity 97.7%; Pred. No. 2.5e-103; Mismatches 3; Indels 0; Gaps 0; Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEOLGARVYIELDNSGETTFSRSEPFPMSTFKVLCGAVSRID 60  
 Db 24 HPETLVVKDAEOLGARVYIELDNSGETTFSRSEPFPMSTFKVLCGAVSRID 60  
 QY 61 AGOEOLGRRIHYSQNDLVEYSPTKEHLDGMVRELSAATMSDNTAANLLTTGGP 120  
 Db 84 AGOEOLGRRIHYSQNDLVEYSPTKEHLDGMVRELSAATMSDNTAANLLTTGGP 120  
 QY 121 KELTAFLHNGDHTRLDRWEPNEAINDERTTTPVAMATLRLKLTGELTLASRQ 180  
 Db 144 KELTAFLHNGDHTRLDRWEPNEAINDERTTTPVAMATLRLKLTGELTLASRQ 203  
 QY 181 QLIDWMEDAKVAGPLRSALPAGFLADKSGAGERSGSGITAAALGPDGKPSRIVVYTG 240  
 Db 204 QLIDWMEDAKVAGPLRSALPAGFLADKSGAGERSGSGITAAALGPDGKPSRIVVYTG 240  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 8

Q93A80 PRELIMINARY; PRT; 286 AA.  
 ID Q93A80 01-DEC-2001 (TREMbirel. 19, Created)  
 AC Q93A80; DT 01-MAR-2003 (TREMbirel. 23, Last sequence update)  
 DT DE Inhibitor-resistant beta-lactamase TEM-81.  
 GN BACTERIA; OS Escherichia coli.  
 OC Bacteria; OC Bacteriia; OC Gammaproteobacteria; OC Enterobacteriales; OC Enterobacteriaceae; OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN RP SEQUENCE FROM N.A.  
 RP RA Hanson N.D., Moland E.S., Pitout J.D.,  
 RX RT "TEM-63, A Novel TEM-type Extended Spectrum Beta-lactamase Expressed  
 RA RT In Three Different Genera of Enterobacteriaceae from South Africa.",  
 RT DR Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 RT DR EMBL: AF32513; AACI17194.1; -.  
 RT DR HSSP: P00810; ITEM:  
 DT DR InterPro: IPR001466; Beta\_lactamase.  
 DE DR InterPro: IPR000871; Beta\_lactamase\_A.  
 PRIM; PR00144; beta-lactamase; 1.  
 DR PROSITE: PRO0118; BLACTAMASE.  
 SQ DR PROSITE: PS00146; BETA\_LACTAMASE\_A; 1.  
 SEQUENCE 286 AA; 31449 NM; ABB60086CE3AEB3 CRC64;

Query Match, 98.2%; Score 1321; DB 2; Length 286;  
 Best Local Similarity 97.7%; Pred. No. 2.5e-103; Mismatches 3; Indels 0; Gaps 0; Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEOLGARVYIELDNSGETTFSRSEPFPMSTFKVLCGAVSRID 60  
 Db 24 HPETLVVKDAEOLGARVYIELDNSGETTFSRSEPFPMSTFKVLCGAVSRID 60  
 QY 61 AGOEOLGRRIHYSQNDLVEYSPTKEHLDGMVRELSAATMSDNTAANLLTTGGP 120  
 Db 84 AGOEOLGRRIHYSQNDLVEYSPTKEHLDGMVRELSAATMSDNTAANLLTTGGP 120  
 QY 121 KELTAFLHNGDHTRLDRWEPNEAINDERTTTPVAMATLRLKLTGELTLASRQ 180  
 Db 144 KELTAFLHNGDHTRLDRWEPNEAINDERTTTPVAMATLRLKLTGELTLASRQ 203  
 QY 181 QLIDWMEDAKVAGPLRSALPAGFLADKSGAGERSGSGITAAALGPDGKPSRIVVYTG 240  
 Db 204 QLIDWMEDAKVAGPLRSALPAGFLADKSGAGERSGSGITAAALGPDGKPSRIVVYTG 240  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9

Q9AGJ5 PRELIMINARY; PRT; 286 AA.  
 ID Q9AGJ5 01-JUN-2001 (TREMbirel. 17, Created)  
 AC Q9AGJ5; DT 01-JUN-2001 (TREMbirel. 17, Last sequence update)  
 DT DR Extended spectrum beta-lactamase TEM-63.  
 DE BLATEM-63.  
 OS Escherichia coli.  
 OC Bacteria; OC Bacteriia; OC Gammaproteobacteria; OC Enterobacteriales; OC Enterobacteriaceae; OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN RP SEQUENCE FROM N.A.  
 RP RA Hanson N.D., Moland E.S., Pitout J.D.,  
 RX RT "TEM-63, A Novel TEM-type Extended Spectrum Beta-lactamase Expressed  
 RA RT In Three Different Genera of Enterobacteriaceae from South Africa.",  
 RT DR Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 RT DR EMBL: AF32513; AACI17194.1; -.  
 RT DR HSSP: P00810; ITEM:  
 DT DR InterPro: IPR001466; Beta\_lactamase.  
 DE DR InterPro: IPR000871; Beta\_lactamase\_A.  
 PRIM; PR00144; beta-lactamase; 1.  
 DR PROSITE: PRO0118; BLACTAMASE.  
 SQ DR PROSITE: PS00146; BETA\_LACTAMASE\_A; 1.  
 SEQUENCE 286 AA; 31449 NM; ABB60086CE3AEB3 CRC64;

Query Match, 98.2%; Score 1321; DB 2; Length 286;  
 Best Local Similarity 97.3%; Pred. No. 2.5e-103; Mismatches 4; Indels 0; Gaps 0; Matches 256; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Query Match, 98.2%; Score 1321; DB 2; Length 286;  
 Best Local Similarity 97.3%; Pred. No. 2.5e-103; Mismatches 4; Indels 0; Gaps 0; Matches 256; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEOLGARVYIELDNSGETTFSRSEPFPMSTFKVLCGAVSRID 60  
 Db 24 HPETLVVKDAEOLGARVYIELDNSGETTFSRSEPFPMSTFKVLCGAVSRID 60  
 QY 61 AGOEOLGRRIHYSQNDLVEYSPTKEHLDGMVRELSAATMSDNTAANLLTTGGP 120  
 Db 84 AGOEOLGRRIHYSQNDLVEYSPTKEHLDGMVRELSAATMSDNTAANLLTTGGP 120  
 QY 121 KELTAFLHNGDHTRLDRWEPNEAINDERTTTPVAMATLRLKLTGELTLASRQ 180  
 Db 144 KELTAFLHNGDHTRLDRWEPNEAINDERTTTPVAMATLRLKLTGELTLASRQ 203  
 QY 181 QLIDWMEDAKVAGPLRSALPAGFLADKSGAGERSGSGITAAALGPDGKPSRIVVYTG 240  
 Db 204 QLIDWMEDAKVAGPLRSALPAGFLADKSGAGERSGSGITAAALGPDGKPSRIVVYTG 240  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 10

Q9R435 PRELIMINARY; PRT; 286 AA.  
 ID Q9R435 01-MAY-2000 (TREMbirel. 13, Created)  
 AC Q9R435; DT 01-MAY-2000 (TREMbirel. 13, Last sequence update)  
 DT DR 01-OCT-2003 (TREMbirel. 25, Last annotation update)  
 DE EXTENDED SPECTRUM beta-lactamase.  
 OS Klebsiella pneumoniae.

OG Plasmid pKKC0-2.

OC Bacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.

OX NCBI\_TaxID=573;

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=RMK107;

RC Cho D.T.; Shin H.S.;

RA "Molecular Evolution of blaTEM of Extended Spectrum of beta-lactamase (ESBL) in Klebsiella pneumoniae isolated in Korea.";

RT Submitted (ISEB-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NEB65;

RA Povart C., Mugnier P., Quesnes G., Berche P., Trieu-Cuot P.;

RT "A novel extended-spectrum TEM-type beta-lactamase from Klebsiella pneumoniae hydrolyzing Moxalactam.";

RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF027199; AAB84239.1; -.

DR EMBL; Y13612; CAA7933.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

DR InterPro; IPR01466; Beta\_lactamase.

DR InterPro; IPR00871; Beta\_lactamase\_A.

DR Pfam; PF00144; beta-lactamase; 1.

DR PRINTS; PRO0118; BLACTAMASE.

DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.

KW Plasmid.

SQ SEQUENCE 286 AA; 31514 MW; 13717ACCB58F6FB6 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;

Best local Similarity 97.7%; Pred. No. 2.5e-103; Indels 0; Gaps 0;

Matches 257; Conservative 3; Mismatches 2; MisMatches 4; Indels 0; Gaps 0;

QY 1 HPETLVKVDAEDQIGARVGYIELDINSGETLESRSEERPPMMSTFKVILCGAVLRSID 60

QY 24 HEILVVKVQDAEDQIGARVGYIELDINSGETLESRSEERPPMMSTFKVILCGAVLRSID 83

QY 61 AGQEQLGRRTIHYSONDLVVEYSPVTEKHLTDGMTRBLCSAITSMSDNTAANLLTIGP 120

QY 84 AGQEQLGRRTIHYSONDLVVEYSPVTEKHLTDGMTRBLCSAITSMSDNTAANLLTIGP 143

Db 121 KELTAFLHNNGDHVRLDRWPEPELNEAPENDERDTTPVAMATRKLLGELLTASRQ 180

Db 144 KELTAFLHNNGDHVRLDRWPEPELNEAPENDERDTTPVAMATRKLLGELLTASRQ 203

QY 181 QLIDWMEADKVAQPLRSALPGWFLADKSGAGERGRSGRGTIAALGPDGKSRIVIYTG 240

Db 204 QLIDWMEADKVAQPLRSALPGWFLADKSGAGERGRSGRGTIAALGPDGKSRIVIYTG 263

QY 241 SQATMDERNRQIAETGASLIKHW 263

Db 264 SQATMDERNRQIAETGASLIKHW 286

RESULT 12

Q8K0M4 PRELIMINARY; PRT; 286 AA.

ID Q8K0M4 PRELIMINARY; PRT; 286 AA.

AC Q8K0M4; 1

DT 01-OCT-2002 (TREMBrel. 22, Created)

DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)

DE TEM-93 ES-beta-lactamase.

GN BLA-TEM-93.

OS Escherichia coli.

OG Plasmid pBlTEM-93.

OC Bacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI\_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=CLSI 3445/98;

RC Gniadkowski M.;

RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A./\*

RC STRAIN=CLSI 3445/98;

RA Baranik A.;

RT "Evolution of TEM extended-spectrum beta-lactamases in Poland.";

RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ318093; CACB5560.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

DR InterPro; IPR01466; Beta\_lactamase.

DR InterPro; IPR00871; Beta\_lactamase\_A.

DR Pfam; PF00144; beta-lactamase; 1.

DR PRINTS; PRO0118; BLACTAMASE.

DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.

KW Plasmid.

SQ SEQUENCE 286 AA; 31514 MW; 1555DCE499016FB8 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;

Best local similarity	97.7%	Pred.	No.	2.5e-103;
Matches	257;	Conservative	3;	Mismatches 3;
Indels	0;	Gaps	0;	
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 13				
QKRS3				
PRELIMINARY;		PRT;	286 AA.	
AC	QKRS3			
DR	01-OCT-2002 (TREMbrel. 22, Created)			
DT	01-JUN-2003 (TREMbrel. 22, Last sequence update)			
DB	01-JUN-2003 (TREMbrel. 24, Last annotation update)			
OS	Beta-lactamase TEM-104.			
OC	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Klebsiella.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	SIRAIN-SM91;			
RA	Edelstein M.V.;			
RT	"sequence diversity of the genes encoding broad-spectrum TEM-type beta-lactamases in clinical Escherichia coli strains. ";			
RT	Submitted (SRP-1999) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: AP188199; AAF01046.1; -.			
DR	HSRP; P00810; IKB.			
DR	InterPro; IPR001466; Beta_lactamase.			
DR	InterPro; IPR000871; Beta_lactamase_A.			
DR	pfam; PF00144; beta-lactamase_1.			
DR	PRINTS; PRO0118; BLACTAMASE.			
FT	PROSITE; PS00145; BETA_LACTAMASE_A; 1.			
FT	VARIANT 202- 202 Q->R.			
SQ	SEQUENCE 286 AA; 31487 MW; B864BA43B9776BD9 CRC64;			
QY	Query Match 98.2%; Score 1321; DB 2; Length 286;			
QY	Best Local Similarity 97.7%; Pred. No. 2.5e-103;			
Matches	257;	Conservative	3;	Mismatches 3;
Indels	0;	Gaps	0;	
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 15				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 16				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 17				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 18				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 19				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 20				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 21				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 22				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 23				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 24				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 25				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		
RESULT 26				
QY	1	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 60		
Db	24	HPETLWVVKVKAEDQLGARVGYIELDINGSKLIESFRPEERIPMMSTPKVILGAVLSRID 83		
QY	61	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 120		
Db	84	AGQEBQGRRIYHSQNDLVEVSPTVERKLTDTQVTELCSAITSMSNTAANLLTIGP 143		
QY	121	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 180		
Db	144	KELTAFLHNMGDHVTLDRMPELNAHPNEDRTTPVAMATURKLLTGEILLTASRQ 203		
QY	181	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 240		
Db	204	QOLIDWMEADKVGAGPLRSALPAGWFTADKSGAGERSRGITAAALGPDGKRSRIVVYTG 263		
QY	241	SOATMDERNQIAETGASLIKHW 263		
Db	264	SOATMDERNQIAETGASLIKHW 286		

RA Rosenau A., Cattier B., Gousset P., Harriau P., Philippon A.,  
 RA Quentin R.;  
 RT "Capnocytophaga ochracea: characterization of a plasmid-encoded  
 extended-spectrum TEM-17 beta-lactamase in the phylum Flavobacter-  
 RT Bacteroides";  
 RL Antimicrob. Agents Chemother. 44:760-762 (2000).  
 DR EMBL; Y14574; CAA74912.2; -.  
 DR HSSP; P00830; 1XB.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR InterPro; IPR000871; Beta\_lactamase\_A.  
 DR Pfam; PF00144; beta-lactamase; 1.  
 DR PRINS; PRO0118; BLACTAMASE.  
 DR PRSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
 DR Sequence; 286 AA; 31514 MW; BD498F6B9D369345 CRC64;  
 SQ

Query Match 98.2%; Score 1321; DB 2; Length 286;  
 Best Local Similarity 97.7%; Pred. No. 2,5e-103;  
 Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 保守性 3; 错配 3; 缺失 0; 插入 0;

QY 1 HPTETLVKDAEDEIGARVGYIELDINGEILSFRSERFPMNSTFKVLLCGAVLSRID 60  
 Db 24 HPTETLVKDAEDEIGARVGYIELDINGEILSFRSERFPMNSTFKVLLCGAVLSRID 83

QY 61 AGEQOLGRIGRHYSONDLVKGVPTEKHLTDGMWVYRELCSAATMSDNTAANLITGGP 120  
 Db 84 AGEQOLGRIGRHYSONDLVKGVPTEKHLTDGMWVYRELCSAATMSDNTAANLITGGP 143

QY 121 KELTAFLHMGHVTLDWEPPELINEATPNDERTITPAMATIRKLTGELITLRSQ 180  
 Db 144 KELTAFLHMGHVTLDWEPPELINEATPNDERTITPAMATIRKLTGELITLRSQ 203

QY 181 QLIDMEADKVAGPLRSALPAGWFLADSGAGERGSRGIAALGPDGKPSRIVIYITG 240  
 Db 204 QLIDMEADKVAGPLRSALPAGWFLADSGAGERGSRGIAALGPDGKPSRIVIYITG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 26  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

Search completed: June 18, 2004, 19:10:01  
 Job time : 47 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.									
OM protein - protein search, using sw model									
Run on: June 18, 2004, 18:27:53 ; Search time 60 Seconds (without alignments)									
EPPER526106.PEP									
Title: Perfect score: 1345									
Sequence: 1 hpetlvkvkdaedqigargv.....tdemrnrqiaeigaslikhw 263									
Scoring table: BIOTSUM62									
Gapop 10.0 , Gapext 0.5									
Searched: 1586107 seqs, 283547505 residues									
Total number of hits satisfying chosen parameters: 1586107									
Minimum DB seq length: 0									
Maximum DB seq length: 2000000000									
Post-processing: Minimum Match 0% Maximum Match 100%									
Listing first 45 summaries									
Database : A_Geneseq_29Jan04:*									
1: geneseq291980s:*									
2: geneseq2000s:*									
3: geneseq2001s:*									
4: geneseq2002s:*									
5: geneseq2003s:*									
6: geneseq2003bs:*									
7: geneseq2004s:*									
8: geneseq2004bs:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description	Key	Location/Qualifiers		
1	1330	98.9	263	4 AAB50544	aae0554 E. coli m	RESULT 1	/note= "Break-point between alpha and omega fragments"		
2	1330	98.9	263	4 AAB36692	hab36692 Escherich	ID AAB05544	/note= "standard; protein; 263 AA."		
3	1330	98.9	264	2 AAW16634	haw16634 Beta-lact	XX	/note= "Inter-sub-domain loop"		
4	1330	98.9	264	2 AAW18680	haw18680 Intracell	XX	/note= "Break-point between alpha and omega fragments"		
5	1330	98.9	286	2 AAB31575	har31575 Ampicillin	XX	/note= "Break-point between alpha and omega fragments"		
6	1330	98.9	286	2 AAB97619	har97619 Secretory	XX	/note= "Break-point between alpha and omega fragments"		
7	1330	98.9	286	2 AAB96423	cyclohexam	XX	/note= "Break-point between alpha and omega fragments"		
8	1330	98.9	286	2 AAW16635	haw16635 Beta-lact	XX	/note= "Break-point between alpha and omega fragments"		
9	1330	98.9	286	2 AAW18679	haw18679 Secretory	XX	/note= "Break-point between alpha and omega fragments"		
10	1330	98.9	286	2 AAY08529	haw08529 Vector pa	XX	/note= "Break-point between alpha and omega fragments"		
11	1330	98.9	286	3 AAB10442	hab10442 Expressio	XX	/note= "Break-point between alpha and omega fragments"		
12	1330	98.9	286	3 AAB10438	hab10438 Expressio	XX	/note= "Break-point between alpha and omega fragments"		
13	1330	98.9	286	3 AAB10440	hab10440 Expressio	XX	/note= "Break-point between alpha and omega fragments"		
14	1330	98.9	286	4 AAB50898	hab50988 Protein e	FT	/note= "Break-point between alpha and omega fragments"		
15	1330	98.9	286	4 AAB31173	hab31173 Amino aci	FT	/note= "Break-point between alpha and omega fragments"		
16	1330	98.9	286	5 AAB75511	hab7551 celz inte	FT	/note= "Break-point between alpha and omega fragments"		
17	1330	98.9	286	6 ABB55474	abb55474 Vector pc	FT	/note= "Break-point between alpha and omega fragments"		
18	1330	98.9	286	6 ABB43622	abb43622 Cloning v	XX	/note= "Break-point between alpha and omega fragments"		
19	1330	98.9	290	4 AAB23219	hab23219 Novel hum	DN	/note= "Break-point between alpha and omega fragments"		
20	1330	98.9	290	4 AABW4362	habw4362 Human imm	XX	/note= "Break-point between alpha and omega fragments"		
21	1330	98.9	327	2 AAW16636	haw16636 Beta-lact	XX	/note= "Break-point between alpha and omega fragments"		
22	1330	98.9	327	2 AAW18681	haw18681 Membrane-	XX	/note= "Break-point between alpha and omega fragments"		
23	1330	98.9	408	6 ABB55981	abb55981 HCC beta-	XX	/note= "Break-point between alpha and omega fragments"		
24	1330	98.9	585	6 AAB67747	ada67747 Beta-lact	PR	/note= "Break-point between alpha and omega fragments"		
25	1330	98.9	1088	2 AAB88636	hab88636 Plasmid p	PR	/note= "Break-point between alpha and omega fragments"		

XX (PANO-) PANORAMA RES INC.  
 PA XX (PANO-) PANORAMA RES INC.  
 XX PI  
 XX Balint RF, Her J;  
 XX DR WPI; 2001-451857/48.  
 DR N-PSDB; AAD10411.  
 XX PT  
 PT Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permuted PT proteins.  
 XX PT  
 PS Claim 38; Fig 2; 104pp; English.  
 XX  
 CC The invention relates to new interaction-dependent enzyme association (IDEA) systems that comprise a fusion sequence that encodes for a circularly permuted, interaction-activated proteins that reassemble to form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon simultaneous association of two oligopeptides with a third oligopeptide. The marker protein is preferably a type A beta-lactamase, especially TEM-1 beta-lactamase of *Escherichia coli*. The oligopeptide is a member of a proteome library selected from single chain antibody Fv fragment library, an antibody light chain variable region library and a peptide library, displayed within thioredoxin. The IDEA systems are useful for detecting and identifying interactions between intracellular as well as extracellular proteins, particularly between two or three polypeptides. The systems are also useful in selecting with a single marker protein the incorporation of multiple genetic traits in a host cell. In particular, the systems are useful in many applications in human therapeutics, diagnostics and prognostics, as well as in high-throughput screening systems for the discovery and validation of pharmaceutical targets and drugs. Prior systems (e.g. E. coli Dimer Detection System, Yeast two-hybrid system or Selective Infective Phage System) require multiple steps between interaction and phenotype, which cause severe loss of efficiency due to high false positive and false negative rates. The present system is capable of simultaneous detection of multiple interactions between extra-cellular as well as intracellular proteins in a high throughput format. The circularly permuted marker proteins comprising interaction-dependent enzymes find use in cell-based sensors for activation or inhibition of metabolic or signal transduction pathways, in high-throughput mapping of pair-wise protein-protein interactions within and between the proteomes of cells, tissues and pathogenic organisms, and in cell-based screens for high-throughput selection of inhibitors of any protein-protein interaction. The present sequence is *Escherichia coli* mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-lactamase is a product of ampicillin resistance gene. The enzyme has two domains, alpha-omega and mu  
 CC domains, alpha-omega and mu  
 XX Sequence 263 AA:  
 Query Match 98.9%; Score 1330; DB 4; Length 263;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-129;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 SQ  
 CC 1 HPEETLVKVKDAEDQLGARVGYIELDNSGETILESFRSEERTPMMSTPKVILCGAVLSRID 60  
 CC 1 HETELVVKVKDAEDQLGARVGYIELDNSGKLESFRPEERPPMSIFPKVILCGAVLSRID 60  
 CC 61 AGQEOLGRRHYSQNDLVEVSPVTEKHLTDGTMVRELSGSAITMSNTAANLLTIGGP 120  
 CC 61 AGQEOLGRRHYSQNDLVEVSPVTEKHLTDGTMVRELSGSAITMSNTAANLLTIGGP 120  
 Db 121 KELTAFLHNMGHVTDRWEPPELNEAIPNDRDTTPVAMATTKLKLGELLTASRQ 180  
 Db 121 KELTAFLHNMGHVTDRWEPPELNEAIPNDRDTTPVAMATTKLKLGELLTASRQ 180  
 QY 1 HPEETLVKVKDAEDQLGARVGYIELDNSGETILESFRSEERTPMMSTPKVILCGAVLSRID 60  
 QY 1 HPEETLVKVKDAEDQLGARVGYIELDNSGETILESFRSEERTPMMSTPKVILCGAVLSRID 60  
 Db 181 QLIDWMEADKVGAPLRSALPGWFLADKSGAERGSRGIAITALGDGKSRIVIYTG 240  
 Db 181 QLIDWMEADKVGAPLRSALPGWFLADKSGAERGSRGIAITALGDGKSRIVIYTG 240  
 QY 241 SQATMDERNRQARIGASLIKHW 263

Do 241 SQATMDERNRQARIGASLIKHW 263

RESULT 2  
 PI AAB36692  
 XX ID AAB36692 standard; protein; 263 AA.  
 AC AAB36692;  
 XX DT 15-MAR-2001 (first entry)  
 XX DE Escherichia coli mature TEM-1 beta-lactamase protein sequence.  
 XX KW Interaction-activated protein; beta-lactamase; protein interaction.  
 XX OS *Escherichia coli*.  
 XX PN WO200071702-A1.  
 XX PR 25-MAY-1999; 9905-01359262.  
 XX PR 13-JAN-2000; 2000US-01759681.  
 XX PA (PANO-) PANORAMA RES INC.  
 XX PI Balint RF, Her J;  
 XX DR WPI; 2001-032034/04.  
 DR N-PSDB; AAC90773.  
 XX PT  
 PT Novel fragment complementation system to identify interactions between PT polypeptides comprises fragment pairs having first and second members PT that reassemble into a marker protein which has a directly detectable signal.  
 XX  
 PS Disclosure; Fig 2; 94pp; English.  
 XX  
 CC The present invention describes a fragment complementation system (I) which comprises a first oligopeptide (OPI) containing an N-terminal fragment with a C-terminal break point and a second oligopeptide (OPI2) comprising a C-terminal with a N-terminal breakpoint, in which the C and N terminal fragments are both derived from a marker protein (MP). Methods from the present invention are used for monitoring the occurrence of protein-protein interactions in a sample, identifying oligopeptide interactions between two different proteomes, identifying epitopes that bind to an immunoglobulin (Ig) variable region, for identifying interactions between an extracellular domain of a transmembrane protein and a polypeptide, for high-throughput identification of compounds that inhibit phosphorylation-regulated signal transducers, forming a enzyme complementation system for selecting simultaneous incorporation of multiple genetic elements into a host cell and for activating a beta-lactam derivative of an antibiotic or the *Escherichia coli* mature TEM-1 beta-lactamase, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 263 AA:  
 Query Match 98.9%; Score 1330; DB 4; Length 263;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-129;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 SQ  
 CC 1 HPEETLVKVKDAEDQLGARVGYIELDNSGETILESFRSEERTPMMSTPKVILCGAVLSRID 60  
 CC 1 HPEETLVKVKDAEDQLGARVGYIELDNSGETILESFRSEERTPMMSTPKVILCGAVLSRID 60  
 Db 61 AGQEOLGRRHYSQNDLVEVSPVTEKHLTDGTMVRELSGSAITMSNTAANLLTIGGP 120  
 Db 61 AGQEOLGRRHYSQNDLVEVSPVTEKHLTDGTMVRELSGSAITMSNTAANLLTIGGP 120





Query Match	98.9%	Score	1330;	DB	2;	Length	286;
Best Local Similarity	98.9%	Pred.	No.	2.2e-129;			
Matches	260;	Conservative	1;	Mismatches	2;	Indels	0;
						Gaps	0;
QY	1	HPETLVKVQDAEDOLGARVGYIELDNSGILESFRSEERFPFMSTFKVILCGAVLSRID					
Db	24	HPETLVKVQDAEDOLGARVGYIELDNSGILESFRSEERFPFMSTFKVILCGAVLSRID					
QY	61	AGEQOLGRRHYSONDLYVEYSPTEKHLTDGMVRELCSAITMSDNIAANLLITIGP					
Db	84	AGEQOLGRRHYSONDLYVEYSPTEKHLTDGMVRELCSAITMSDNIAANLLITIGP					
QY	121	KELTAFLHNGDHTVRLDRWEPELNEATPNDERDTTPVAMATTIRKLTGELITLASRQ					
Db	144	KELTAFLHNGDHTVRLDRWEPELNEATPNDERDTTPVAMATTIRKLTGELITLASRQ					
QY	181	QLIDWMEADKVGAPLRLSALPAGFIADKSGAGERGRSGRSGITIAALGPDGKPSRIVIYTG					
Db	204	QLIDWMEADKVGAPLRLSALPAGFIADKSGAGERGRSGRSGITIAALGPDGKPSRIVIYTG					
QY	241	SOATMDERNRQIAETGASLIKHW	263				
Db	264	SOATMDERNRQIAETGASLIKHW	286				
RESULT	7						
ID	AAR96423	standard; protein; 286 AA.					
AC	AAR96423;						
XX							
DT	25-MAR-2003	(revised)					
DT	25-NOV-1996	(first entry)					
DB	Cytochrome P450 (CYP1A1 construct).						
XX							
KW	cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;						
XX							
OS	Homo sapiens.						
PN	US5525482-A.						
XX							
PD	11-JUN-1996.						
XX							
PF	15-NOV-1994;	94US-00339658.					
XX							
PR	27-JUN-1991;	91US-00721775.					
XX							
PR	09-DEC-1992;	92US-00990295.					
XX							
PA	(TYWA-) UNIV WAYNE STATE.						
XX							
PT	Hines RN, Novak RF, States JC;						
XX							
DR	WPI: 1996-286397/29.						
DR	N-PSDB; AAT30354.						
XX							
PT	Testing chemicals for cytotoxicity to human by detecting gene damage - using recombinant fibroblasts transformed with cytochrome P450 gene under control of inducible promoter.						
XX							
PS	Disclosure; Col 17-24; 26pp; English.						
XX							
CC	The present sequence is encoded by a chimeric mouse metallothionein- cytochrome P450 <sub>1A1</sub> (CYP1A1) expression construct. Two clones, pRNH127 and pRNH15, were isolated by different methods and which both had the same sequence. The CYP1A1 construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially toxic chemicals. The cells having been transformed to express cytochrome P450, under the control of a controllable promoter through the CYP1A1 gene, upon exposure to the chemical in vitro. The chemical is metabolised						
CC							
CC	Molecular chimaera for gene or virus directed enzyme prodrug therapy - useful for treatment of cancer, viral infection or inflammation.						
CC	Example; Page 26; 38pp; English.						
BS	Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide, is the expression product of a molecular chimaera, designated pCMV-delBL, (AAW6738), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional						

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for  
 CC enzyme prodrug therapy. Intracellular expression of the beta-lactamase in  
 CC a targeted cell allows conversion of a prodrug into an agent toxic to  
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or  
 CC inflammation.

XX Sequence 286 AA;

Query Match 99.9%; Score 1330; DB 2; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 2.2e-129; 1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 260; Conservative 1;

QY 1 HPERILVKVDAEOLGARGVYIELDNSGELLSFRSEERFPMSITFKVILCGAVLSRID 60  
 24 HPERILVKVDAEOLGARGVYIELDNSGELLSFRSEERFPMSITFKVILCGAVLSRID 83

QY 61 AGEBOLGRHYSNDLYVEYSYPTVEKHLTDGMVTRELCSAATMSDNIAANLILITGGP 120  
 84 AGEBOLGRHYSNDLYVEYSYPTVEKHLTDGMVTRELCSAATMSDNIAANLILITGGP 143

QY 121 KELTAFLHMGDHVTRLDWPELNEAIPNDERDTTPYAMATTIRKLTGELITLASKQ 180  
 144 KELTAFLHMGDHVTRLDWPELNEAIPNDERDTTPYAMATTIRKLTGELITLASKQ 203

QY 181 QLIDWMEADKVAGLRLSALPAGMFIADKSGAGBERGSRGITAALGPDKPSRIVIYTG 240  
 204 QLIDWMEAKVAGLRLSALPAGMFIADKSGAGBERGSRGITAALGPDKPSRIVIYTG 263

QY 241 SQATMDERNRQIAETGASLKH 263

Db 264 SQATMDERNRQIAETGASLKH 286

RESULT 9  
 AAWI8679  
 ID AAWI8679 standard; protein; 286 AA.

AC AAWI8679;

XX  
 DT 13-AUG-1997 (first entry)

DR Secretory beta-lactamase.

XX  
 KW Prodrug therapy; gene directed enzyme prodrug therapy; GDEPT;  
 KW virus directed enzyme prodrug therapy; VDEPT; lung cancer;  
 KW beta-lactamase; PCMV-BL.

XX  
 OS Escherichia coli.

XX  
 FH Location/Qualifiers  
 FT Peptide 1. .23  
 FT /label= sig\_peptide  
 FT 24. .286  
 FT /label= Mat\_protein

XX  
 PN WO9719183-A2.

XX  
 PD 29-MAY-1997.

XX  
 PR 19-NOV-1996; 96WO-GB002846.

XX  
 PR 20-NOV-1995; 95GB-00023703.

XX  
 PA (GLAX ) GLAXO GROUP LTD.

XX  
 PI Dev I, Moore JT, Sethna PB;

XX  
 DR WPI; 1997-298118/27.

XX  
 DR N-PSDB; AAV70309.

XX  
 PT DNA construct for gene-directed enzyme prodrug therapy of lung cancer -  
 PT comprises lung- or neuroendocrine-specific promoter controlling  
 PT expression of prodrug-converting enzyme.

XX Sequence 286 AA;

Query Match 99.9%; Score 1330; DB 2; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 2.2e-129; 1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 260; Conservative 1;

QY 1 HPERILVKVDAEOLGARGVYIELDNSGELLSFRSEERFPMSITFKVILCGAVLSRID 60  
 24 HPERILVKVDAEOLGARGVYIELDNSGELLSFRSEERFPMSITFKVILCGAVLSRID 83

QY 61 AGEBOLGRHYSNDLYVEYSYPTVEKHLTDGMVTRELCSAATMSDNIAANLILITGGP 120  
 84 AGEBOLGRHYSNDLYVEYSYPTVEKHLTDGMVTRELCSAATMSDNIAANLILITGGP 143

QY 121 KELTAFLHMGDHVTRLDWPELNEAIPNDERDTTPYAMATTIRKLTGELITLASKQ 180  
 144 KELTAFLHMGDHVTRLDWPELNEAIPNDERDTTPYAMATTIRKLTGELITLASKQ 203

QY 181 QLIDWMEADKVAGLRLSALPAGMFIADKSGAGBERGSRGITAALGPDKPSRIVIYTG 240  
 204 QLIDWMEAKVAGLRLSALPAGMFIADKSGAGBERGSRGITAALGPDKPSRIVIYTG 263

QY 241 SQATMDERNRQIAETGASLKH 263

Db 264 SQATMDERNRQIAETGASLKH 286

RESULT 10  
 AAYO8529  
 ID AAYO8529 standard; protein; 286 AA.

AC AAYO8529;

XX  
 DT 03-AUG-1999 (first entry)

XX  
 DE Vector pASK75 beta-1a protein.

XX  
 KW Firstly; luciferase; tetracycline; transcriptional control; TetR; TetA;  
 KW tetracycline repressor; tetracycline promoter; luminescence; luxCDBB;  
 KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;  
 KW allergy.

XX  
 OS Synthetic.

XX  
 PN WO925866-A1.

XX  
 PD 27-MAY-1999.

XX  
 PR 11-NOV-1998; 98WO-FI000873.

XX  
 PR 14-NOV-1997; 97FI-00004235.

XX  
 PA (KORP) KORPELA M.

PA (KARP) KARP M.

PA (KURI) KURITTU J.

XX  
 PI Korpela M, Karp M, Kurittu J;

XX  
 DR WPI; 1999-338015/28.

XX  
 DR N-PSDB; AAV72418.

XX  
 PT Assaying for tetracycline using recombinant prokaryotic cells.

XX  
PS Disclosure; Page 47-48; 67pp; English.  
XX  
CC This invention describes a novel tetracycline assay that uses recombinant  
CC prokaryotic cells comprising a luciferase gene under the transcriptional  
CC control of a tetracycline repressor and tetracycline promoter and  
CC involves the detection of luminescence emitted from the cells. The assay  
CC can be used to distinguish tetracycline from other microbial agents. The assay  
CC invention also describes a novel plasmid comprising either the luxCDABE  
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (Teta)  
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)  
CC and a tetracycline promoter (Teta) from Tn10. The tetracycline assay  
CC method can be used for the determination of tetracycline in a sample,  
CC e.g. to study the dosage and penetration of the medicine. The method can  
CC also be used to test cheese production, as cheese making bacteria are not  
CC able to work in the presence of tetracycline. The method can also be used  
CC to determine the presence or concentration of antibiotics in foodstuffs,  
CC e.g. for allergic people. The present assay method does not rely on the  
CC growth of microbes as do conventional tests, and so is much more rapid.  
CC The present assay is also more sensitive, as even a small amount of  
CC luminescence can be detected  
XX  
SQ Sequence 286 AA;  
Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Db 24 HPTELVKYKDAEDOLGARGVYIYELDNGSGLLESFRSRERFPMSTEKVILCGAVLNSID 60  
QY 1 HPTELVKYKDAEDOLGARGVYIYELDNGSGLLESFRSRERFPMSTEKVILCGAVLNSID 60  
Db 84 AGOBOLGRRIHYSONDLVEYSPVTEKHLTDGMVTRELCSAITSNDNPAANLITTCGP 143  
QY 24 HPTELVKYKDAEDOLGARGVYIYELDNGSGLLESFRSRERFPMSTEKVILCGAVLNSID 63  
Db 121 KELTAFLHMGDHTDRWEPPELNEALPNDERDTTVMAMTTRKLTGELTLASRQ 180  
QY 144 KELTAFLHMGDHTDRWEPPELNEALPNDERDTTVMAMTTRKLTGELTLASRQ 180  
Db 181 QLIDWMEADKVAQPLRSALPAGMFIADKSAGAERGRSGRGIATAALGPDGKPSRIVWVYTG 240  
QY 204 QLIDWMEADKVAQPLRSALPAGMFIADKSAGAERGRSGRGIATAALGPDGKPSRIVWVYTG 263  
Db 241 SQATMDERNRQIAEIGASLIKHW 263  
QY 264 SQATMDERNRQIAEIGASLIKHW 286  
RESULT 11  
AAB10442 ID AAB10442 standard; protein; 286 AA.  
XX  
AC AAB10442;  
XX  
DT 01-DEC-2000 (first entry)  
XX  
DB Expression vector pSEK15G2 bla protein.  
XX  
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;  
XX  
OS Synthetic.  
XX  
PN DR1990635 A1.  
PD 13-JUL-2000.  
XX  
PF 11-JAN-1999; 99DE-01000635.  
XX  
PR 11-JAN-1999; 99DE-01000635.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
XX  
PI Breitling F, Poustka A, Moldenhauer G;  
XX  
DR WPI; 2000-499832/45.  
XX  
PT N-PSDB; AAA71430.  
XX  
PT Selecting monoclonal antibodies, by expressing them on the surface of  
PT hybridomas attached to antibody-binding protein, then reaction with  
PT antibody library.  
XX  
PS Claim 16; Fig 3; 22pp; German.  
XX  
CC This invention describes a novel method for the selection of monoclonal  
CC antibodies (Mab) which comprises (i) fusing B Lymphocytes with myeloma  
CC cells to produce antibody-producing hybridomas such that the antibodies  
CC are presented at the surface of the hybridomas by an antibody-binding  
CC protein (I); and (ii) binding the antibody to antigens (Ag). The  
CC invention also describes antibody-binding proteins (I) that comprise a  
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa  
CC chain or a murine MHC (major histocompatibility complex) Class I (kappa)  
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the  
CC transmembrane domain of PDGF (platelet-derived growth factor receptor)  
CC or CD52. The method is used to select Mab with specificity for particular  
CC antigens. Mab can be selected without separate culture of hybridomas, and  
CC selection can be made against many antigens in a library, optionally on  
CC the basis of strength of affinity for a particular antigen. Complex  
mixtures of hybridomas can be used for selection, reducing the time and  
CC cost involved in Mab selection. This sequence represents the bla protein  
CC contained in the expression vector pSEK15G2 which contains the  
XX  
SQ Sequence 286 AA;  
Query Match 98.9%; Score 1330; DB 3; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Db 24 HPTELVKYKDAEDOLGARGVYIYELDNGSGLLESFRSRERFPMSTEKVILCGAVLNSID 60  
QY 1 HPTELVKYKDAEDOLGARGVYIYELDNGSGLLESFRSRERFPMSTEKVILCGAVLNSID 60  
Db 84 AGOBOLGRRIHYSONDLVEYSPVTEKHLTDGMVTRELCSAITSNDNPAANLITTCGP 143  
QY 61 AGOBOLGRRIHYSONDLVEYSPVTEKHLTDGMVTRELCSAITSNDNPAANLITTCGP 120  
Db 84 AGOBOLGRRIHYSONDLVEYSPVTEKHLTDGMVTRELCSAITSNDNPAANLITTCGP 143  
QY 121 KELTAFLHMGDHTDRWEPPELNEALPNDERDTTVMAMTTRKLTGELTLASRQ 180  
Db 181 QLIDWMEADKVAQPLRSALPAGMFIADKSAGAERGRSGRGIATAALGPDGKPSRIVWVYTG 240  
QY 204 QLIDWMEADKVAQPLRSALPAGMFIADKSAGAERGRSGRGIATAALGPDGKPSRIVWVYTG 263  
Db 241 SQATMDERNRQIAEIGASLIKHW 263  
QY 264 SQATMDERNRQIAEIGASLIKHW 286  
RESULT 12  
AAB10438 ID AAB10438 standard; protein; 286 AA.  
XX  
AC AAB10438;  
XX  
DT 01-DEC-2000 (first entry)  
XX  
DB Expression vector pSEK111 bla protein.  
XX  
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;  
XX  
OS Synthetic.  
XX





QY 61 AGCBOGLGRTHYSQNDLVYSPTPEKHLTDGMWTRELCSAALTMSDNATAANLITIGGP 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 84 AGCBOGLGRRIHYSQNDLVYSPTPEKHLTDGMWTRELCSAALTMSDNATAANLITIGGP 143  
 QY 121 KELTAFLRNGDVTTRLWRPEPLNEALPNDEDUTTIVAMATLTKLITGEELITLASRQ 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 144 KELTAFLRNGDVTTRLWRPEPLNEALPNDEDUTTIVAMATLTKLITGEELITLASRQ 203  
 Db 181 QLDDWMEADKVAGLLRSLPAGMFLAKSGAERGSRGILIAALGPDKPSRIVIYTG 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 204 QLDDWMEADKVAGPLRSLPAGMFLAKSGAERGSRGIIAALGPDKPSRIVIYTG 263  
 QY 241 SQATMDERNQIAITGASLIKHW 263  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 264 SQATMDERNQIAITGASLIKHW 286

Search completed: June 18, 2004, 19:08:00  
 Job time : 63 secs

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:08:33 ; Search time 20 Seconds  
(Without alignments)

Scoring table: BLSSDM62

Gapop 10.0 , Gapext 0.5

Searched: 294345 seqs, 45236911 residues

Total number of hits satisfying chosen parameters: 294345

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New: \*

1: //cgn2\_6/ptodata/2/paa/PCT NEW COMB.pep: \*

2: //cgn2\_6/ptodata/2/paa/US06 NEW COMB.pep: \*

3: //cgn2\_6/ptodata/2/paa/US07 NEW COMB.pep: \*

4: //cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep: \*

5: //cgn2\_6/ptodata/2/paa/US09 NEW COMB.pep: \*

6: //cgn2\_6/ptodata/2/paa/US10 NEW COMB.pep: \*

7: //cgn2\_6/ptodata/2/paa/US60 NEW COMB.pep: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	1330	98.9	286	5	US-09-490-324-265 Sequence 265, APP Sequence 362, APP
2	1330	98.9	286	5	US-09-490-324-362 Sequence 73, APP
3	1330	98.9	286	6	US-10-416-708A-73 Sequence 523, APP
4	1330	98.9	286	6	US-10-045-674A-523 Sequence 285, APP
5	1330	98.9	299	5	US-09-420-324-285 Sequence 299, APP
6	1330	98.9	299	5	US-09-420-324-298 Sequence 300, APP
7	1329	98.8	286	6	US-10-842-534-300 Sequence 9, APP
8	1329	98.8	1293	6	US-10-668-035-57 Sequence 57, APP
9	1318	98.8	265	6	US-10-622-089-114 Sequence 114, APP
10	1302	95.8	498	6	US-10-491-653-146 Sequence 146, APP
11	343.5	25.5	306	6	US-10-734-972A-6154 Sequence 6154, APP
12	175	13.0	290	6	US-10-442-522-65 Sequence 65, APP
13	137	10.2	334	6	US-10-453-372-332 Sequence 332, APP
14	137	10.2	841	6	US-10-453-372-334 Sequence 334, APP
15	109	8.1	21	6	US-10-453-372-334 Sequence 334, APP
16	107.5	8.0	524	6	US-10-414-532-28 Sequence 146, APP
17	107.5	8.0	524	6	PCT-US04-12717-118 Sequence 118, APP
18	102	7.6	432	1	US-10-831-070-118 Sequence 118, APP
19	102	7.6	432	6	US-10-60-546-745-58 Sequence 58, APP
20	102	7.6	432	7	US-60-556-841-6264 Sequence 6264, APP
21	98	7.3	550	7	US-60-556-841-6264 Sequence 3455, APP
22	98	7.3	552	7	US-60-556-841-3455 Sequence 761, APP
23	95.5	7.1	561	6	US-10-796-280-761 Sequence 90, APP
24	94.5	7.0	410	6	US-10-474-792-90 Sequence 406, APP
25	6.7	507	7	US-10-556-841-406 Sequence 101, APP	
26	6.7	1217	1	PCT-US04-02188-101	

**ALIGNMENTS**

RESULT 1

US-09-490-324-265

Sequence 265, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Illeg, Vic

Ge, Liming

Moroney, Simon

Pineckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

ZIP: 10021

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILED DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILED DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILED DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-324-265

Query Match 98.9%: Score 1330: DB 5: Length 286.

Best Local Similarity 98.9%; Pred. No. 1.7e-11; Indels 0; Gaps 0; Matches 260; Conservative 1; Mismatches 0;

Sequence 362, Application US/09490324  
 GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 Pack, Peter  
 Illeg, Vic  
 Ge, Liming  
 Moroney, Simon  
 Pueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 COMPUTER: Floppy disk  
 MEDIUM: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 APPLICATION NUMBER: US/09/490,324  
 FILING DATE: 24-Jan-2000  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769  
 FILING DATE: 18-FEB-1998  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 362:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 286 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 362:  
 US-09-490-324-362

Best Matches	Local 260;	Similarity 98.9%;	Pred. No. 1.1e-115;	1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	HPETLVKVKDAEDQIGARGVGIELDINSGETESFRSEERPPMMSTPKVILCGAVLSRID	60				
Db	24	HPETLVKVKDAEDQIGARGVGIELDINSGETESFRSEERPPMMSTPKVILCGAVLSRID	83				
Qy	61	AGQEQLGRRHYSQNDLVEYSPTEKHLTDGMVTEHLCSAATMSDNTAANTLTTIGGP	120				
Qy	84	AGQEQLGRRHYSQNDLVEYSPTEKHLTDGMVTEHLCSAATMSDNTAANTLTTIGGP	143				
Db	121	KELTAFLAHNMGDHVTULDRWPEPLMAIPNDRDTTPVAMATIRKLUTGELITLRSQ	180				
Qy	144	KELTAFLAHNMGDHVTULDRWPEPLMAIPNDRDTTPVAMATIRKLUTGELITLRSQ	203				
Db	181	QLIDWMERADKVGAGPLRSALLAGWFTADKSGAGERSRSRGTIALGDKPSRIVVYITG	240				
Qy	204	QLIDWMERADKVGAGPLRSALLAGWFTADKSGAGERSRSRGTIALGDKPSRIVVYITG	263				
Qy	241	SQATMDERNRQIAEGASLIKW	253				
Db	264	SQATMDERNRQIAEGASLIKW	286				

```

US-10-416-708A-73
; Sequence 73, Application US/10416708A
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; TITLE OF INVENTION: SPECIFICITIES
; FILE REFERENCE: 37179-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 73
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; US-10-416-708A-73

Query Match: 98.9%; Score: 1330; DB: 6; Length: 286;
Best Local Similarity: 98.9%; Pred. No: 1..7e-119; 2; Mismatches: 1; Indexes: 0; Gaps: 0;
Matches: 260; Conservative: 1; Mismatches: 2; Indexes: 0; Gaps: 0;

QY 1 HPETIIVKVKDAEDQIGARYGYIELDINSRILESFRSERFPMSTFKULLCGAVLSRID 60
Db 24 HPETIIVKVKDAEDQIGARYGYIELDINSRILESFRSERFPMSTFKULLCGAVLSRID 83
QY 61 AGQERGLGRRIHYSONDLVYSPVKEKHLTGMVTRFLCSAINTMSDNATANLILITIGGP 120
Db 84 AGQEQGRRHYSONDLVYSPVKEKHLTGMVTRFLCSAINTMSDNATANLILITIGGP 143
QY 121 KELTATLHNNGDHYTRLDWEPELENAIENDERUTTPYAMATIRKLTGELLTASRQ 160
Db 144 KELTATLHNNGDHYTRLDWEPELENAIENDERUTTPYAMATIRKLTGELLTASRQ 203
QY 181 QLIDMWMEADKVAGPILRSALPAGWIAIDSGAGERGSRGLIAAIGPDKPSRIVWVYTG 240
Db 204 QLIDMWMEADKVAGPILRSALPAGWIAIDSGAGERGSRGLIAAIGPDKPSRIVWVYTG 263
QY 241 SOATMDERNRQIAETGASLTKHW 283
Db 264 SQATMDERNRQIAETGASLIKHW 286

RESULT 4
US-10-045-674A-523

```

GENERAL INFORMATION:  
 APPLICANT: LADNER, ROBERT C.  
 APPLICANT: COHEN, EDWARD H.  
 APPLICANT: NASTRI, HORACIO G.  
 APPLICANT: ROOKY, KRISTIN L.  
 APPLICANT: HOET, RENE  
 APPLICANT: HOGENBOOM, HENDRICKUS R. J. M.  
 CURRENT APPLICATION NUMBER: US/10/045,674A  
 CURRENT FILING DATE: 2001-10-25  
 PRIORITY APPLICATION NUMBER: 05/198,069  
 PRIORITY FILING DATE: 2000-04-17  
 PRIORITY APPLICATION NUMBER: 09/837,306  
 PRIORITY FILING DATE: 2001-04-17  
 NUMBER OF SEQ ID NOS: 635  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 523  
 LENGTH: 286  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS  
 US-10-045-674A-523

Query Match 98.9%; Score 1330; DB 6; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 1.7e-19; Mismatches 1; Indels 0; Gaps 0;  
 Matches 260; Conservative 1; MisMatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEQLGARVGYIELDINGEELSFSEERFPMSFKVLLGCAVLRSID 60  
 Db 24 HPETLVVKDAEQLGARVGYIELDINGEELSFSEERFPMSFKVLLGCAVLRSID 83

QY 61 AGOEQLGRRHYSQNDLVEYSPTKEHLTDGMVRELSAITSMSDNIAANLLITGGP 120  
 Db 84 AGOEQLGRRHYSQNDLVEYSPTKEHLTDGMVRELSAITSMSDNIAANLLITGGP 143

QY 121 KELTAFLINNGHVTDRWEPBLNEALPNDERDTTVAAMATTLKLTGELITLSRQ 180  
 Db 144 KELTAFLINNGHVTDRWEPBLNEALPNDERDTTVAAMATTLKLTGELITLSRQ 203

QY 181 QLIDWMEADKVAGPLRSALPAGWFIADKSAGGERGSRGIAALGPDKPSRIVWYTG 240  
 Db 204 QLIDWMEADKVAGPLRSALPAGWFIADKSAGGERGSRGIAALGPDKPSRIVWYTG 263

QY 241 SOATMDERNRQABIGASLIKW 263  
 Db 264 SOATMDERNRQABIGASLIKW 286

RESULT 5  
 US-09-490-324-285  
 ; Sequence 285, Application US/09490324  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knapik, Achim  
 ; Packer, Peter  
 ; Ilag, Vic  
 ; Ge, Liming  
 ; Moroney, Simon  
 ; Blueckhun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021

Query Match 98.9%; Score 1330; DB 5; Length 299;  
 Best Local Similarity 98.9%; Pred. No. 1.9e-11; Mismatches 1; Indels 0; Gaps 0;  
 Matches 260; Conservative 1; MisMatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKDAEQLGARVGYIELDINGEELSFSEERFPMSFKVLLGCAVLRSID 60  
 Db 24 HPETLVVKDAEQLGARVGYIELDINGEELSFSEERFPMSFKVLLGCAVLRSID 83

QY 61 AGOEQLGRRHYSQNDLVEYSPTKEHLTDGMVRELSAITSMSDNIAANLLITGGP 120  
 Db 84 AGOEQLGRRHYSQNDLVEYSPTKEHLTDGMVRELSAITSMSDNIAANLLITGGP 143

QY 121 KELTAFLINNGHVTDRWEPBLNEALPNDERDTTVAAMATTLKLTGELITLSRQ 180  
 Db 144 KELTAFLINNGHVTDRWEPBLNEALPNDERDTTVAAMATTLKLTGELITLSRQ 203

QY 181 QLIDWMEADKVAGPLRSALPAGWFIADKSAGGERGSRGIAALGPDKPSRIVWYTG 240  
 Db 204 QLIDWMEADKVAGPLRSALPAGWFIADKSAGGERGSRGIAALGPDKPSRIVWYTG 263

QY 241 SOATMDERNRQABIGASLIKW 263  
 Db 264 SOATMDERNRQABIGASLIKW 286

RESULT 6  
 US-09-490-324-298  
 ; Sequence 298, Application US/09490324  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knapik, Achim  
 ; Packer, Peter  
 ; Ilag, Vic  
 ; Ge, Liming  
 ; Moroney, Simon  
 ; Blueckhun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA: US/09/490,324

FILING DATE: 24-Jan-2000

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 298:

SEQUENCE CHARACTERISTICS:

LENGTH: 299

MOLECULE TYPE: amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 298:

US-09-490-324-298

Query Match 98.9%; Score 1330; DB 5; Length 299;

Best Local Similarity 98.9%; Pred. No. 1.9e-119; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

\*Qy 1 HPETLVVKVDAEDQGARGVYIELDNSGILESFRSERFRPMSTFKVILCGAVLSRID 60

Db 24 HPETLVVKVDAEDQGARGVYIELDNSGILESFRSERFRPMSTFKVILCGAVLSRID 83

\*Qy 61 AGQEQLGRRHYSQNDLVYSPVTEKHLTDGMTRELCSAITSNTAANLLTTGGP 120

Db 84 AGQEQLGRRHYSQNDLVYSPVTEKHLTDGMTRELCSAITSNTAANLLTTGGP 143

\*Qy 121 KELTAFLHNNGDHVTRLDRWEPELNEAIPNDRDTTPVAMATTURKLTGELLTASRQ 180

Db 144 KELTAFLHNNGDHVTRLDRWEPELNEAIPNDRDTTPVAMATTURKLTGELLTASRQ 203

\*Qy 181 QLIDWNEADKVAGPLRSALPAGWFLADSKGAGERSGSGTIAAGPDGKPSRIVVYTG 240

Db 204 QLIDWNEADKVAGPLRSALPAGWFLADSKGAGERSGSGTIAAGPDGKPSRIVVYTG 263

\*Qy 241 SQATMDERNRQIAETGASLIKHW 263

Db 264 SQATMDERNRQIAETGASLIKHW 286

RESULT 7 US-09-490-324-300

; Sequence 300, Application US/09490324

; GENERAL INFORMATION:

; APPLICANT: Knapik, Achim

; Pack, Peter

; Tilag, Vic

; Ge, Liming

; Moroney, Simon

; Pluckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave

STREET: 1231 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA: US/09/490,324

FILING DATE: 24-Jan-2000

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 300:

SEQUENCE CHARACTERISTICS:

LENGTH: 299 amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 300:

US-09-490-324-300

Query Match 98.9%; Score 1330; DB 5; Length 299;

Best Local Similarity 98.9%; Pred. No. 1.9e-119; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

\*Qy 1 HPETLVVKVDAEDQGARGVYIELDNSGILESFRSERFRPMSTFKVILCGAVLSRID 60

Db 24 HPETLVVKVDAEDQGARGVYIELDNSGILESFRSERFRPMSTFKVILCGAVLSRID 83

\*Qy 61 AGQEQLGRRHYSQNDLVYSPVTEKHLTDGMTRELCSAITSNTAANLLTTGGP 120

Db 84 AGQEQLGRRHYSQNDLVYSPVTEKHLTDGMTRELCSAITSNTAANLLTTGGP 143

\*Qy 121 KELTAFLHNNGDHVTRLDRWEPELNEAIPNDRDTTPVAMATTURKLTGELLTASRQ 180

Db 144 KELTAFLHNNGDHVTRLDRWEPELNEAIPNDRDTTPVAMATTURKLTGELLTASRQ 203

\*Qy 181 QLIDWNEADKVAGPLRSALPAGWFLADSKGAGERSGSGTIAAGPDGKPSRIVVYTG 240

Db 204 QLIDWNEADKVAGPLRSALPAGWFLADSKGAGERSGSGTIAAGPDGKPSRIVVYTG 263

\*Qy 241 SQATMDERNRQIAETGASLIKHW 263

Db 264 SQATMDERNRQIAETGASLIKHW 286

RESULT 8 US-10-842-534-9

; Sequence 9, Application US/10842534

; GENERAL INFORMATION:

; APPLICANT: Stewart, Francis

; APPLICANT: Zhang, Youming

; APPLICANT: Buchholz, Frank

; TITLE OF INVENTION: NOVEL DNA CLONING METHOD

; FILE REFERENCE: 2933-618

; CURRENT APPLICATION NUMBER: US/10/842,534

; PRIOR FILING DATE: 2004-05-11

; PRIOR APPLICATION NUMBER: US 10/231,013

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: US 09/555,510

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: PCT/EP 98/07945

; PRIOR FILING DATE: 1998-12-07

; PRIOR APPLICATION NUMBER: EP 97121462.2

; PRIOR FILING DATE: 1997-12-05

PRTOR APPLICATION NUMBER: EP 98118756.0  
 PRIORITY FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 9  
 LENGTH: 286  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: DOMAIN  
 ; LOCATION: (1)..(286)  
 ; OTHER INFORMATION: bla gene on plasmid PBAD24-recent at 3493-4353  
 US-10-842-534-9

Query Match 98.8%; Score 1329; DB 6; Length 286;  
 Best Local Similarity 98.5%; Pred. No. 2.2e-119; Matches 259; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKYKDAEQLGARVGYELDINGRILESFRSEERFPMSTFKVILCGAVSLRID 60  
 Db 245 HPETLVVKYKDAEQLGARVGYELDINGRILESFRSEERFPMSTFKVILCGAVSLRID 304

QY 61 AGEQOLGRRIRHQSNDLVEYSPTEKHTIDGMVRELCASAITMSDNTAANLLITIGGP 120  
 Db 305 AGEQOLGRRIRHQSNDLVEYSPTEKHTIDGMVRELCASAITMSDNTAANLLITIGGP 364

QY 121 KELTAFLHNGDHVTRLDRWEPINEALPNDERDTTPEVAMATTIRKLUTGELITLRSQ 180  
 Db 365 KELTAFLHNGDHVTRLDRWEPINEALPNDERDTTPEVAMATTIRKLUTGELITLRSQ 424

QY 181 QLIDWMRAKDVAPLRLSALPAWFLAKSGAERGRGSGIIALGPOOKPSKIVIWTG 240  
 Db 425 QLIDWMRAKDVAPLRLSALPAWFLAKSGAERGRGSGIIALGPOOKPSKIVIWTG 484

QY 241 SQATMDERNRQAHIGASLIKHW 263  
 Db 485 SQATMDERNRQAHIGASLIKHW 507

RESULT 9  
 US-10-668-035-57

; Sequence 57, Application US/10668035

; GENERAL INFORMATION:  
 ; APPLICANT: Behan, Dominic P.  
 ; APPLICANT: Chalmers, Derek T.  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Lin, I-Lin  
 ; APPLICANT: Lowitz, Kevin P.  
 ; APPLICANT: Chen, Ruoping  
 ; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled  
 ; CURRENT FILING DATE: 2003-09-22  
 ; PRIORITY FILING DATE: 1998-07-31  
 ; PRIORITY FILING NUMBER: US 60/106,300  
 ; PRIORITY FILING DATE: 1998-10-30  
 ; PRIORITY FILING NUMBER: US 60/110,906  
 ; PRIORITY FILING DATE: 1998-12-04  
 ; PRIORITY FILING NUMBER: US 60/121,851  
 ; PRIORITY FILING DATE: 1998-02-26  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 57  
 ; LENGTH: 1293  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-668-035-57

Query Match 98.8%; Score 1329; DB 6; Length 1293;  
 Best Local Similarity 98.5%; Pred. No. 1.8e-18; Matches 259; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVVKYKDAEQLGARVGYELDINGRILESFRSEERFPMSTFKVILCGAVSLRID 60  
 Db 3 HPETLVVKYKDAEQLGARVGYELDINGRILESFRSEERFPMSTFKVILCGAVSLRID 62

QY 61 AGEQOLGRRIRHQSNDLVEYSPTEKHTIDGMVRELCASAITMSDNTAANLLITIGGP 120  
 Db 63 AGEQOLGRRIRHQSNDLVEYSPTEKHTIDGMVRELCASAITMSDNTAANLLITIGGP 122

QY 121 KELTAFLHNGDHVTRLDRWEPINEALPNDERDTTPEVAMATTIRKLUTGELITLRSQ 180  
 Db 123 KELTAFLHNGDHVTRLDRWEPINEALPNDERDTTPEVAMATTIRKLUTGELITLRSQ 182

RESULT 11  
 US-10-491-653-146  
 Sequence 146, Application US/10491653  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Breitling, Frank  
 ; APPLICANT: Moldenhauer, Gerhard  
 ; APPLICANT: Poistka, Annemarie  
 ; APPLICANT: Kuijtgau, Sandra  
 ; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins  
 ; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins  
 ; FILE REFERENCE: 4121-162  
 ; CURRENT APPLICATION NUMBER: US/10/491,653  
 ; CURRENT FILING DATE: 2004-04-01  
 ; PRIOR APPLICATION NUMBER: EP 01123596.7  
 ; PRIOR FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/10852  
 ; PRIOR FILING DATE: 2002-09-27  
 ; NUMBER OF SEQ ID NOS: 151  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 146  
 ; LENGTH: 498  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Construct  
 ; US-10-491-653-146

Query Match 96.8%; Score 1302; DB 6; Length 498;  
 Best Local Similarity 98.5%; Pred. No. 1.8e-116; Matches 257; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 ETLVKVKDAEDQGLARGVYIELDNSGETIERSFSEEREFMMSPKVILGAVSIRDAG 62  
 Db 238 BTLVKVKDAEDQGLARGVYIELDNSGETIERSFSEEREFMMSPKVILGAVSIRDAG 297

QY 63 QEQGLGRRIHSQNDLVEYSPTVKEHITDGMTVRELCSAATMSDNTAANLLTIGGKE 122  
 Db 298 QEQGLGRRIHSQNDLVEYSPTVKEHITDGMTVRELCSAATMSDNTAANLLTIGGKE 357

QY 123 LTAFLHNMGDIVTRLDWERPELNEAPNDRDTTPVAMATTRLKLTGELLTASRQQL 182  
 Db 358 LTAFLHNMGDIVTRLDWERPELNEAPNDRDTTPVAMATTRLKLTGELLTASRQQL 417

QY 183 FDWMERDKVAGFLPSALPAGFWIADKGSGAGERGSRGITALGPGKPSIVIVITGSO 242  
 Db 418 IDTIMEADKVGFLPSALPAGFWIADKGSGAGERGSRGITALGPGKPSIVIVITGSO 477

QY 243 ATMDERNQTAEGASLIKW 263  
 Db 478 ATMDERNQTAEGASLIKW 498

RESULT 12  
 US-10-724-972A-6154  
 ; Sequence 6154, Application US/10724972A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Duquette-Saam, Lynn  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: PATH03-16  
 ; CURRENT APPLICATION NUMBER: US/10/724,972A

Query Match 13.0%; Score 175; DB 6; Length 290;  
 Best Local Similarity 24.1%; Pred. No. 6.7e-09; Matches 76; Conservative 38; Mismatches 101; Indels 100; Gaps 10;  
 QY 1 HPTETLVKVKDAEDQGLA-RVGYIELDNSGETIERSFSEEREFMMSPKVILGAVSIR 58  
 Db 244 HPTETLVKVKDAEDQGLA-RVGYIELDNSGETIERSFSEEREFMMSPKVILGAVSIR 81

RESULT 13  
 US-10-414-532-65  
 Sequence 532, Application US/10414532  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CURTISS III, ROY  
 ; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING  
 ; TITLE OF INVENTION: CARRIER BACTERIA THAT SEcrete ANTIGENS  
 ; FILE REFERENCE: 56202-40437  
 ; CURRENT APPLICATION NUMBER: US/10/414,532  
 ; CURRENT FILING DATE: 2003-04-15  
 ; PRIOR APPLICATION NUMBER: 60/372,710  
 ; PRIOR FILING DATE: 2002-04-16  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO: 65  
 ; LENGTH: 290  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Protein  
 ; OTHER INFORMATION: sequence of blast-pspA-EP5668-bla C-term region in  
 ; OTHER INFORMATION: DIA3637  
 ; US-10-414-532-65



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